GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 06:44:49 ; Search time 2545 Seconds
(without alignments)
9504.270 Million cell updates/sec

Title: US-09-852-100B-1
Perfect score: 810
Sequence: 1 atgcatattttaaaagggtc.....aaacgcaattatatccataa 810

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	673	83.1	678	12	BG702759	BG702759 602684629
2	643.8	79.5	836	12	BG723403	BG723403 602694073
3	642.8	79.4	788	14	CB996712	CB996712 AGENCOURT
4	636.4	78.6	658	12	BG709182	BG709182 602675061
5	635	78.4	982	11	BC048995	BC048995 Homo sapi
6	631.6	78.0	750	12	BI458114	BI458114 603198535
7	626.2	77.3	975	12	BI546941	BI546941 603190155
8	622.4	76.8	882	12	BI464436	BI464436 603205310
9	621.6	76.7	879	12	BI462204	BI462204 603205517
10	613.4	75.7	615	13	BQ639765	BQ639765 he20a04.y
11	606.4	74.9	772	14	CB310671	CB310671 AGENCOURT
12	606	74.8	950	12	BI562596	BI562596 603256530
13	605.4	74.7	901	12	BI596830	BI596830 603243323
14	604.4	74.6	908	12	BI596662	BI596662 603243232
15	595.4	73.5	599	9	AI923178	AI923178 wn67b10.x
16	587.4	72.5	788	14	CB229262	CB229262 AGENCOURT
17	576.8	71.2	775	14	CB311691	CB311691 AGENCOURT
18	572.4	70.7	574	9	AI680904	AI680904 tx42f05.x
19	571	70.5	961	10	BF968960	BF968960 602270156
20	556	68.6	943	13	BQ232033	BQ232033 AGENCOURT
21	555	68.5	556	9	AI479764	AI479764 tm69b04.x
22	547	67.5	547	10	BE467256	BE467256 hz63f03.x
23	534	65.9	534	10	BE467235	BE467235 hz63d03.x
24	531.2	65.6	537	9	AI580361	AI580361 tm47h02.x
25	530.8	65.5	534	10	BE328144	BE328144 ht97f11.x
26	527.4	65.1	530	9	AI674462	AI674462 wc44e01.x
27	521.4	64.4	523	12	BM698864	BM698864 UI-E-DX1-
28	516	63.7	516	10	BE348755	BE348755 ht70b01.x
29	513.8	63.4	542	12	BG700625	BG700625 602682226
30	513.4	63.4	548	9	AA772225	AA772225 ai41c01.s
31	513.4	63.4	771	13	BX108300	BX108300 BX108300
32	506	62.5	507	9	AI682204	AI682204 wa71b06.x
33	503.6	62.2	603	9	AV654663	AV654663 AV654663
34	497	61.4	498	9	AI349520	AI349520 qp72g05.x
35	495.6	61.2	526	10	BE549799	BE549799 7b38g08.x
36	494.4	61.0	506	14	CB122011	CB122011 K-EST0169
37	492.8	60.8	500	9	AI680969	AI680969 tx35h07.x
38	476	58.8	870	14	CB993944	CB993944 AGENCOURT
39	475.2	58.7	799	12	BG701162	BG701162 602680739
40	474.6	58.6	586	14	CB430834	CB430834 606754 MA
41	472.8	58.4	808	14	CB991349	CB991349 AGENCOURT
42	471.2	58.2	830	14	CB992200	CB992200 AGENCOURT
43	466.2	57.6	791	14	CA451757	CA451757 UI-M-FX0-
44	464	57.3	891	10	BF692101	BF692101 602247882
45	459.2	56.7	922	13	BQ876648	BQ876648 AGENCOURT

ALIGNMENTS

RESULT 1
BG702759
LOCUS BG702759 678 bp mRNA linear EST 07-MAY-2001
DEFINITION 602684629F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4817358 5', mRNA sequence.
ACCESSION BG702759
VERSION BG702759.1 GI:13974418
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 678)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10717 row: i column: 07
High quality sequence stop: 678.
FEATURES Location/Qualifiers
source 1. .678
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4817358"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_95"
/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
ORIGIN

Query Match 83.1%; Score 673; DB 12; Length 678;
Best Local Similarity 100.0%; Pred. No. 4.7e-175;
Matches 673; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        135 GCTCCTGGGCGGAGGCGGAAGCGGAAGTGGCGAGAAAGTGTCGGTCTCCAAGATGGCGGC 194
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Db          6 GCTCCTGGGCGGAGGCGGAAGCGGAAGTGGCGAGAAAGTGTCGGTCTCCAAGATGGCGGC 65

Qy        195 CGCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGCCAGACTCGTTGGTGTCCT 254
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 CGCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGCCAGACTCGTTGGTGTCCT 125

Qy        255 GTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCTGTTGCCACCTCCGCCGGGGGCGA 314
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCTGTTGCCACCTCCGCCGGGGGCGA 185

Qy        315 GGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAAAAT 374
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 GGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAAAAT 245

Qy        375 AAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTGTTT 434
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Db        246 AAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTGTTT 305

Qy        435 TCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGGGAA 494
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Db        306 TCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGGGAA 365

Qy        495 CGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAAAGT 554
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 CGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAAAGT 425

Qy        555 GGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGGATA 614
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Db        426 GGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGGATA 485

Qy        615 CCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCTAAT 674
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Db        486 CCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCTAAT 545

Qy        675 TGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACATTAT 734
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Db        546 TGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACATTAT 605

Qy        735 AGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAAAAC 794
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Db        606 AGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAAAAC 665

Qy        795 GCAATTATATCCA 807
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RESULT 2
BG723403
LOCUS BG723403 836 bp mRNA linear EST 08-MAY-2001
DEFINITION 602694073F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4826035 5', mRNA sequence.
ACCESSION BG723403
VERSION BG723403.1 GI:14002590

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KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 836)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10740  row: b  column: 20
            High quality sequence stop: 760.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:4826035"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_97"
                     /note="Organ: testis; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
                     (gtcgag); Oligo-dT primed using primer
                     5'-TTTTTTTTTTTTTTTVN-3', size-selected for  average
                     insert size 2.2 kb and normalized to ROT 5. This is a
                     primary library enriched for full-length clones and
                     constructed using the Cap-trapper method (Carninci, in
                     preparation).  Library constructed by M. Brownstein
                     (NIMH/NHGRI, National Institutes of Health). Note: this is
                     a NIH_MGC Library."
ORIGIN
```

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  Query Match             79.5%;  Score 643.8;  DB 12;  Length 836;
  Best Local Similarity   99.7%;  Pred. No. 6.2e-167;
  Matches  645;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Db          2 GCGGAAAAGTGTCGGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGG 61

Qy        224 AGGCCGTGACGGCCAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCT 283
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Db         62 AGGCCGTGACGGCCAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCT 121

Qy        284 GGGGGGCTGTTGCCACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAG 343
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Db        122 GGGGGGCTGTTGCCACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAG 181
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Qy        344 TGGGACAATATATTTGTAAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAACT 403
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Db        182 TGGGACAATATATTTGTAAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAACT 241

Qy        404 GTACAAACTACACAGCTCATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGGATT 463
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Db        242 GTACAAACTACACAGCTCATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGGATT 301

Qy        464 CCAGTGGCAATGAAACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTT 523
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Db        302 CCAGTGGCAATGAAACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTT 361

Qy        524 GCCGAAATGTAAATGGCTATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGAT 583
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Qy        584 GGTTGGGAGCAGATCGATTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTTGCA 643
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Qy        644 CTGTAGGGTTTTGTGGAATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGATTG 703
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Db        482 CTGTAGGGTTTTGTGGAATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGATTG 541

Qy        704 TTGGACCTTCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGAC 763
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Db        542 TTGGACCTTCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGAC 601

Qy        764 TGAGTATTACTAATGAAACATTTAGAAAAACGCAATTATATCCATAA 810
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Db        602 TGAGTATTACTAATGAAACATTTAGAAAAACGCAATTATATCCATAA 648


RESULT 3
CB996712
LOCUS       CB996712                 788 bp    mRNA    linear   EST 01-MAY-2003
DEFINITION  AGENCOURT_13627955 NIH_MGC_148 Homo sapiens cDNA clone
            IMAGE:30334410 5', mRNA sequence.
ACCESSION   CB996712
VERSION     CB996712.1  GI:30291232
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 788)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Stefan Hansson
             cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
            and advice from Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
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found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM354 row: j column: 19
High quality sequence stop: 566.

FEATURES Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30334410"
/tissue_type="pre-eclamptic placenta"
/lab_host="DH10B TonA"
/clone_lib="NIH_MGC_148"
/note="Organ: placenta; Vector: pBluescriptR; Site_1: alI-XhoI; Site_2: BamH; Library is oligo-dT primed and directionally cloned using primer 5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-lenght clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 79.4%; Score 642.8; DB 14; Length 788;
Best Local Similarity 99.7%; Pred. No. 1.1e-166;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db         24 CCAGAAAGTGTCGGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGA 83

Qy        225 GGCCGTGACGGCCAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTG 284
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GGCCGTGACGGCCAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTG 143

Qy        285 GGGGGCTGTTGCCACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGT 344
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Db        144 GGGGGCTGTTGCCACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGT 203

Qy        345 GGGACAATATATTTGTAAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAACTG 404
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Db        204 GGGACAATATATTTGTAAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAACTG 263

Qy        405 TACAAACTACACAGCTCATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGGATTC 464
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Db        264 TACAAACTACACAGCTCATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGGATTC 323

Qy        465 CAGTGGCAATGAAACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTG 524
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CAGTGGCAATGAAACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTG 383

Qy        525 CCGAAATGTAAATGGCTATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGATG 584
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 CCGAAATGTAAATGGCTATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGATG 443
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Qy        585 GTTGGGAGCAGATCGATTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTTGCAC 644
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Qy        645 TGTAGGGTTTTGTGGAATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGATTGT 704
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Db        504 TGTAGGGTTTTGTGGAATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGATTGT 563

Qy        705 TGGACCTTCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACT 764
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Db        564 TGGACCTTCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACT 623

Qy        765 GAGTATTACTAATGAAACATTTAGAAAAACGCAATTATATCCATAA 810
              |||||||||||||||||||||||||||||||| |||||||||
Db        624 GAGTATTACTAATGAAACATTTAGAAAAACGCAATTGTATCCATAA 669


RESULT 4
BG709182
LOCUS       BG709182                 658 bp    mRNA    linear   EST 07-MAY-2001
DEFINITION  602675061F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4797782 5',
            mRNA sequence.
ACCESSION   BG709182
VERSION     BG709182.1  GI:13987263
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 658)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10684  row: i  column: 15
            High quality sequence stop: 658.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:4797782"
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                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_96"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
                     (gtcgag); Oligo-dT primed using primer
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5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 78.6%; Score 636.4; DB 12; Length 658;
Best Local Similarity 99.7%; Pred. No. 6.4e-165;
Matches 637; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy        172 GTGTCGGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTG 231
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Db          4 GGGTCGGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTG 63

Qy        232 ACGGCCAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCT 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACGGCCAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCT 123

Qy        292 GTTGCCACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAA 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 GTTGCCACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAA 183

Qy        352 TATATTTGTAAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAAC 411
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Db        184 TATATTTGTAAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAAC 243

Qy        412 TACACAGCTCATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGC 471
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Db        244 TACACAGCTCATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGC 303

Qy        472 AATGAAACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAAT 531
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Db        304 AATGAAACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAAT 363

Qy        532 GTAAATGGCTATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGA 591
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Db        364 GTAAATGGCTATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGA 423

Qy        592 GCAGATCGATTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGG 651
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Db        424 GCAGATCGATTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGG 483

Qy        652 TTTTGTGGAATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCT 711
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Db        484 TTTNGTGGAATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCT 543

Qy        712 TCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATT 771
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Db        544 TCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATT 603

Qy        772 ACTAATGAAACATTTAGAAAAACGCAATTATATCCATAA 810
              ||||||||||||||||||||||||||||||||||||||
Db        604 ACTAATGAAACATTTAGAAAAACGCAATTATATCCATAA 642
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RESULT 5
BC048995

LOCUS BC048995 982 bp mRNA linear HTC 17-DEC-2003
DEFINITION Homo sapiens beta-amyloid binding protein precursor, mRNA (cDNA clone IMAGE:5261702).
ACCESSION BC048995
VERSION BC048995.1 GI:28981340
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 982)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
REFERENCE 2 (bases 1 to 982)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 106 Row: h Column: 9
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 7019328
This clone has the following problem: no 5' EST match.

FEATURES Location/Qualifiers
source 1. .982
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/db_xref="taxon:9606"
/clone="IMAGE:5261702"
/tissue_type="Brain, hippocampus"
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/lab_host="DH10B"
/note="Vector: pBluescript"

ORIGIN

Query Match 78.4%; Score 635; DB 11; Length 982;
Best Local Similarity 99.2%; Pred. No. 1.8e-164;
Matches 638; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db          1 GTAAGTGTCGGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGC 60

Qy        228 CGTGACGGCCAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGG 287
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Db         61 CGTGACGGCCAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGG 120

Qy        288 GGCTGTTGCCACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGG 347
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Db        121 GGCTGTTGCCACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGG 180

Qy        348 ACAATATATTTGTAAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAACTGTAC 407
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Qy        408 AAACTACACAGCTCATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGGATTCCAG 467
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Db        241 AAACTATACAGCTCATGTTTCCTGTTTTCCAGCACACAACATAACTTGTAAGGATTCCAG 300

Qy        468 TGGCAATGAAACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCG 527
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Db        301 TGGCAATGAAACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCG 360

Qy        528 AAATGTAAATGGCTATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTT 587
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Db        361 AAATGTAAATGGCTATTCCTACAAAGTGGCAGTAGCATTGTCTCTTTTTCTTGGATGGTT 420

Qy        588 GGGAGCAGATCGATTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGT 647
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Db        421 GGGAGCAGATCGATTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGT 480

Qy        648 AGGGTTTTGTGGAATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGATTGTTGG 707
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Db        481 AGGGTTTTGTGGAATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGATTGTTGG 540
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Qy        708 ACCTTCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAG 767
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Db        541 ACCTTCAGATGGAAGTAGTTACATTATAGATTACTAAGGAACCAGACTTACAAGACTGAG 600

Qy        768 TATTACTAATGAAACATTTAGAAAAACGCAATTATATCCATAA 810
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Db        601 TATTACTAATGAAACATTTAGAAAAACGCAATTATATCCATAA 643


RESULT 6
BI458114
LOCUS       BI458114                 750 bp    mRNA    linear   EST 21-AUG-2001
DEFINITION  603198535F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5278064 5',
            mRNA sequence.
ACCESSION   BI458114
VERSION     BI458114.1  GI:15248770
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 750)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11702  row: e  column: 09
            High quality sequence stop: 711.
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                     /tissue_type="hypothalamus"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_96"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
                     (gtcgag); Oligo-dT primed using primer
                     5'-TTTTTTTTTTTTTTTVN-3', size-selected for average
                     insert size 2.3 kb and normalized to ROT 5. This is a
                     primary library enriched for full-length clones and
                     constructed using the Cap-trapper method (Carninci, in
                     preparation). Library constructed by M. Brownstein
                     (NIMH/NHGRI, National Institutes of Health). Note: this is
                     a NIH_MGC Library."
ORIGIN
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  Query Match             78.0%;  Score 631.6;  DB 12;  Length 750;
  Best Local Similarity   99.1%;  Pred. No. 1.4e-163;
  Matches  645;  Conservative    0;  Mismatches    5;  Indels    1;  Gaps    1;

Qy        161 GTGGCGAGAAAGTGTCGGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTC 220
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Db          4 GGGGGGAGAAAGTGTCGGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTC 63

Qy        221 CGGAGGCCGTGACGGCCAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGAC 280
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Db         64 CGGAGGCCGTGACGGCCAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGAC 123

Qy        281 CCTGGGGGGGCTGTTGCCACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCA 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 CCTGGGGGGGCTGTTGCCACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCA 183

Qy        341 AAGTGGGACAATATATTTGTAAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTA 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 AAGTGGGACAATATATTTGTAAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTA 243

Qy        401 ACTGTACAAACTACACAGCTCATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGG 460
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Db        244 ACTGTACAAACTACACAGCTCATGTTTCATGTTTTCCAGCACCCAACATAACTTGTAAGG 303

Qy        461 ATTCCAGTGGCAATGAAACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATAT 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 ATTCCAGTGGCAATGAAACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATAT 363

Qy        521 CTTGCCGAAATGTAAATGGCTATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTG 580
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Db        364 CTTGCCGAAATGTAAATGGCTATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTG 423

Qy        581 GATGGTTGGGAGCAGATCGATTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTT 640
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Db        424 GATGGTTGGGAGCAGATCGATTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTT 483

Qy        641 GCACTGTAGGGTTTTGTGGAATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGA 700
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Db        484 GCACTGTAGGGTTTTGTGGAATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGA 543

Qy        701 TTGTTGGACCTTCAGATGGAAGTAGTTACA-TTATAGATTACTATGGAACCAGACTTACA 759
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Db        544 TTGTTGGACCTTCAGATGGAAGTAGTTACATTTATAGATTACTATGGAACCAGACTTACA 603

Qy        760 AGACTGAGTATTACTAATGAAACATTTAGAAAAACGCAATTATATCCATAA 810
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Db        604 AGACTGAGTATTACTAATGAAACATTTAGAAAAACGCAATTATATCCANTA 654


RESULT 7
BI546941
LOCUS       BI546941                975 bp    mRNA    linear   EST 05-SEP-2001
DEFINITION  603190155F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5261748 5',
            mRNA sequence.
ACCESSION   BI546941
VERSION     BI546941.1  GI:15434253
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KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 975)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11659  row: m  column: 13
            High quality sequence stop: 766.
FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_95"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
                     (gtcgag); Oligo-dT primed using primer
                     5'-TTTTTTTTTTTTTTTVN-3', size-selected for  average
                     insert size 2.5 kb and normalized to ROT 5. This is a
                     primary library enriched for  full-length clones and
                     constructed using the Cap-trapper method (Carninci, in
                     preparation).  Library constructed by M. Brownstein
                     (NIMH/NHGRI, National Institutes of Health).  Note: this
                     is a NIH_MGC Library."
ORIGIN

  Query Match             77.3%;  Score 626.2;  DB 12;  Length 975;
  Best Local Similarity   98.6%;  Pred. No. 4.9e-162;
  Matches  642;  Conservative    0;  Mismatches    8;  Indels    1;  Gaps    1;

Qy        160 AGTGGCGAGAAAGTGTCGGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCT 219
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Db          1 AGCGTGGAGTAAGTGTCGGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCT 60

Qy        220 CCGGAGGCCGTGACGGCCAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGA 279
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Db         61 CCGGAGGCCGTGACGGCCAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGA 120

Qy        280 CCCTGGGGGGCTGTTGCCACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTC 339
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Db        121 CCCTGGGGGGCTGTTGCCACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTC 180
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Qy        340 AAAGTGGGACAATATATTTGTAAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTT 399
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Db        181 AAAGTGGGACAATATATTTGTAAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTT 240

Qy        400 AACTGTACAAACTACACAGCTCATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAG 459
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Db        241 AACTGTACAAACTATACAGCTCATGTTTCCTGTTTTCCAGCACACAACATAACTTGTAAG 300

Qy        460 GATTCCAGTGGCAATGAAACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATA 519
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Qy        520 TCTTGCCGAAATGTAAATGGCTATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTT 579
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Db        361 TCTTGCCGAAATGTAAATGGCTATTCCTACAAAGTGGCAGTAGCATTGTCTCTTTTTCTT 420

Qy        580 GGATGGTTGGGAGCAGATCGATTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTT 639
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Db        421 GGATGGTTGGGAGCAGATCGATTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTT 480

Qy        640 TGCACTGTAGGGTTTTGTGGAATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAG 699
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Db        481 TGCACTGTAGGGTTTTGTGGAATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAG 540

Qy        700 ATTGTTGGACCTTCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTACA 759
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Db        541 ATTGTTGGACCTTCAGATGGAAGTAGTTACATTATAGATTACTAAGGAACCAGACTTACA 600

Qy        760 AGACTGAGTATTACTAATGAAACATTTAGAAAAACGCAATTATATCCATAA 810
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Db        601 AGACTGAGTATTACTAATGAAACA-TTAGAAAAACGCAATTATATCCATAA 650
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RESULT 8
BI464436
LOCUS       BI464436                 882 bp    mRNA    linear   EST 21-AUG-2001
DEFINITION  603205310F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5271098 5',
            mRNA sequence.
ACCESSION   BI464436
VERSION     BI464436.1  GI:15255092
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 882)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
```

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11684 row: c column: 03
High quality sequence stop: 759.

FEATURES Location/Qualifiers

source 1. .882
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5271098"
/lab_host="DH10B"
/clone_lib="NIH_MGC_97"
/note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 76.8%; Score 622.4; DB 12; Length 882;
Best Local Similarity 99.5%; Pred. No. 5.4e-161;
Matches 645; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

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Qy        164 GCGAGAAAGTGTCGGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGG 223
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Db          4 GGGAGAAAGTGTCGGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGG 63

Qy        224 AGGCCGTGACGGCCAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCT 283
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Db         64 AGGCCGTGACGGCCAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCT 123

Qy        284 GGGGGGCTGTTGCCACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAG 343
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Db        124 GGGGGGCTGTTGCCACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAG 183

Qy        344 TGGGACAATATATTTGTAAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAACT 403
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Qy        524 GCCGAAATGTAAATGGCTATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGAT 583
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Qy        584 GGTTGGGAGCAGATCGATTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTTGCA 643
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Db        424 GGTTGGGAGCAGATCGATTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTTGCA 483

Qy        644 CTGTAGGGTTTTGTGGAATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGATTG 703
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Db        484 CTGTAGGG-TTTGTGGAATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGATTG 542

Qy        704 TTGGACCTTCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGAC 763
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Qy        764 TGAGTATTACTAATGAAACA-TTTAGAAAAACGCAATTATATCCATAA 810
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RESULT 9
BI462204
LOCUS       BI462204                 879 bp    mRNA    linear   EST 21-AUG-2001
DEFINITION  603205517F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5271077 5',
            mRNA sequence.
ACCESSION   BI462204
VERSION     BI462204.1  GI:15252860
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 879)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11684  row: b  column: 06
            High quality sequence stop: 753.
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                     /clone_lib="NIH_MGC_97"
                     /note="Organ: testis; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
                     (gtcgag); Oligo-dT primed using primer
                     5'-TTTTTTTTTTTTTTTVN-3', size-selected for  average
```

insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 76.7%; Score 621.6; DB 12; Length 879;
Best Local Similarity 98.5%; Pred. No. 8.9e-161;
Matches 638; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

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Qy        164 GCGAGAAAGTGTCGGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGG 223
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Db          4 GGGAGAAAGTGTCGGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGG 63

Qy        224 AGGCCGTGACGGCCAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCT 283
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Db         64 AGGCCGTGACGGCCAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCT 123

Qy        284 GGGGGGCTGTTGCCACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAG 343
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Db        124 GGGGGGCTGTTGCCACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAG 183

Qy        344 TGGGACAATATATTTGTAAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAACT 403
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Qy        404 GTACAAACTACACAGCTCATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGGATT 463
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Db        244 GTACAAACTACACAGCTCATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGGATT 303

Qy        464 CCAGTGGCAATGAAACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTT 523
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Db        304 CCAGTGGCAATGAAACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTT 363

Qy        524 GCCGAAATGTAAATGGCTATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGAT 583
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Qy        584 GGTTGGGAGCAGATCGATTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTTGCA 643
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Db        424 GGTTGGGAGCAGATCGATTTTACCTTGGATTACCCTGCTTGGGTTTGTTAAAGTTTTGCA 483

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Db        484 CTGTAGGGTTCTGTGGAATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGATTG 543

Qy        704 TTGGACCTTCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGAC 763
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Qy        764 TGAGTATTACTAATGAAA-CATTTAGAAAAACGCAATTATATCCATAA 810
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RESULT 10
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LOCUS BQ639765 615 bp mRNA linear EST 15-JUL-2002
DEFINITION he20a04.y1 Human Retina cDNA (Un-normalized, unamplified): hd/he
Homo sapiens cDNA clone he20a04 5', mRNA sequence.
ACCESSION BQ639765
VERSION BQ639765.1 GI:21764224
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 615)
AUTHORS Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A.,
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
TITLE Expressed sequence tag analysis of human retina for the NEIBank
Project: Retbindin, an abundant, novel retinal cDNA and alternative
splicing of other retina-preferred gene transcripts
JOURNAL Mol. Vis. 8 (4), 196-204 (2002)
MEDLINE 22103461
PUBMED 12107411
COMMENT Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 20 row: a column: 04
Seq primer: M13RP1 reverse primer (ABI).
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/clone="he20a04"
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/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Human Retina cDNA (Un-normalized,
unamplified): hd/he"
/note="Organ: Eye; Vector: pSPORT1; Neural retina tissue
was dissected from two 80 year old donors with no observed
eye disease. 100ug of total RNA was used for library
construction. A directionally cloned cDNA library in the
pSPORT1 vector (Life Technologies) was constructed at
Bioserve Biotechnology (Laurel MD) essentially following
the protocols of the SuperScript Plasmid System full
details of which are contained in the manufacturer's
Instruction manual (http://www.lifetech.com/). First
strand synthesis was carried out using a Not I
primer-adapter
[5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)15-3']. EST analysis
was performed on the unamplified library at the NIH
Intramural Sequencing Center (NISC)."
ORIGIN

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  Query Match             75.7%;  Score 613.4;  DB 13;  Length 615;
  Best Local Similarity   99.8%;  Pred. No. 1.5e-158;
  Matches  614;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        193 GCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGCCAGACTCGTTGGTGTC 252
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Qy        253 CTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCTGTTGCCACCTCCGCCGGGGGC 312
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Db         61 CTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCTGTTGCCACCTCCGCCGGGGGC 120

Qy        313 GAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAAA 372
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Qy        373 ATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTGT 432
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Db        181 ATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTGT 240

Qy        433 TTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGGG 492
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Db        241 TTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGGG 300

Qy        493 AACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAAA 552
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Qy        553 GTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGGA 612
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Db        361 GTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGGA 420

Qy        613 TACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCTA 672
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Db        421 TACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCTA 480

Qy        673 ATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACATT 732
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Qy        733 ATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAAA 792
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Db        541 ATAGATTACTATGGGACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAAA 600

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Db        601 ACGCAATTATATCCA 615
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RESULT 11
CB310671
LOCUS   CB310671   772 bp   mRNA   linear   EST 04-MAR-2003
DEFINITION AGENCOURT_11828318 NICHD_Rh_Ov1 Macaca mulatta cDNA clone
            IMAGE:6895132 5', mRNA sequence.
ACCESSION   CB310671
VERSION   CB310671.1 GI:28833385
KEYWORDS   EST.

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SOURCE      Macaca mulatta (rhesus monkey)
  ORGANISM  Macaca mulatta
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
            Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 772)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Eliot Spindel
             cDNA Library Preparation: CLONTECH
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM3162  row: c  column: 03
            High quality sequence stop: 646.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:6895132"
                     /tissue_type="Ovary"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NICHD_Rh_Ov1"
                     /note="Organ: ovary; Vector: pDNR-LIB; Site_1: Sfi I;
                     Site_2: Sfi I; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.0-4.0 kb. Tissue pooled from
                     pre-pubertal, post pubertal sn menopausal monkeys.
                     Constructed by Clontech. Note: this is a NICHD Library."
ORIGIN

  Query Match             74.9%;  Score 606.4;  DB 14;  Length 772;
  Best Local Similarity   96.0%;  Pred. No. 1.4e-156;
  Matches  622;  Conservative    0;  Mismatches   26;  Indels    0;  Gaps    0;

Qy        163 GGCGAGAAAGTGTCGGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCG 222
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Qy        223 GAGGCCGTGACGGCCAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCC 282
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Qy        343 GTGGGACAATATATTTGTAAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAAC 402
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Qy        403 TGTACAAACTACACAGCTCATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGGAT 462
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Qy        463 TCCAGTGGCAATGAAACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCT 522
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Qy        523 TGCCGAAATGTAAATGGCTATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGA 582
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Qy        583 TGGTTGGGAGCAGATCGATTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTTGC 642
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Qy        643 ACTGTAGGGTTTTGTGGAATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGATT 702
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Db        481 ACTGTAGGATTTTGTGGAATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGATT 540

Qy        703 GTTGGACCTTCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGA 762
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Qy        763 CTGAGTATTACTAATGAAACATTTAGAAAAACGCAATTATATCCATAA 810
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Db        601 CTAAGTATTACTAATGAAACATATAGAAAAACGCAATTATATCCATAA 648
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RESULT 12
BI562596
LOCUS       BI562596                950 bp    mRNA    linear   EST 05-SEP-2001
DEFINITION  603256530F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5298943 5',
            mRNA sequence.
ACCESSION   BI562596
VERSION     BI562596.1  GI:15449910
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 950)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11756  row: k  column: 08
            High quality sequence stop: 753.
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                     /note="Organ: testis; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
                     (gtcgag); Oligo-dT primed using primer
                     5'-TTTTTTTTTTTTTTTTVN-3', size-selected for  average
                     insert size 2.2 kb and normalized to ROT 5. This is a
                     primary library enriched for full-length clones and
                     constructed using the Cap-trapper method (Carninci, in
                     preparation).  Library constructed by M. Brownstein
                     (NIMH/NHGRI, National Institutes of Health). Note: this is
                     a NIH_MGC Library."
ORIGIN

  Query Match             74.8%;  Score 606;  DB 12;  Length 950;
  Best Local Similarity   98.6%;  Pred. No. 1.9e-156;
  Matches  643;  Conservative    0;  Mismatches    5;  Indels    4;  Gaps    3;

Qy        161 GTGGCGAGAAAGTGTCGGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTC 220
              | ||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 GGGGCGTGAAAGTGTCGGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTC 63

Qy        221 CGGAGGCCGTGACGGCCAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGAC 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 CGGAGGCCGTGACGGCCAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGAC 123

Qy        281 CCTGGGGGGGCTGTTGCCACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCA 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 CCTGGGGGGCTGTTGCCACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCA 183

Qy        341 AAGTGGGACAATATATTTGTAAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTA 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 AAGTGGGACAATATATTTGTAAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTA 243

Qy        401 ACTGTACAAACTACACAGCTCATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGG 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 ACTGTACAAACTACACAGCTCATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGG 303

Qy        461 ATTCCAGTGGCAATGAAACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATAT 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 ATTCCAGTGGCAATGAAACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATAT 363

Qy        521 CTTGCCGAAATGTAAATGGCTATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTG 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 CTTGCCGAAATGTAAATGGCTATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTG 423

Qy        581 GATGGTTGGGAGCAGATCGATTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTT 640
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        424 GATGGTTGGGAGCAGATCGATTTTACCTTGGATACCCTGC-TTGGGTTTGTTAAAGTTTT 482

Qy        641 GCACTGTAGGGTTTTGTGGAATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCA-- 698
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                ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 GCACTGTAGGG-TTTGTGGAATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAAG 541

Qy        699 GATTGTTGGACCTTCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTAC 758
                | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 ATTGGTTGGACCTTCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTAC 601

Qy        759 AAGACTGAGTATTACTAATGAAACATTTAGAAAAACGCAATTATATCCATAA 810
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Db        602 AAGACTGAGTATTACTAATGAAACATTTAGAAAAACGCAATTATATCCATAA 653


RESULT 13
BI596830
LOCUS       BI596830                901 bp    mRNA    linear   EST 07-SEP-2001
DEFINITION  603243323F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5285933 5',
            mRNA sequence.
ACCESSION   BI596830
VERSION     BI596830.1  GI:15489769
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 901)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11722  row: m  column: 06
            High quality sequence stop: 760.
FEATURES             Location/Qualifiers
     source          1. .901
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                     /mol_type="mRNA"
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                     /clone="IMAGE:5285933"
                     /tissue_type="hypothalamus"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_96"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
                     (gtcgag); Oligo-dT primed using primer
                     5'-TTTTTTTTTTTTTTTVN-3', size-selected for  average
                     insert size 2.3 kb and normalized to ROT 5. This is a
                     primary library enriched for full-length  clones and
                     constructed using the Cap-trapper method (Carninci, in
                     preparation).  Library constructed by M. Brownstein
```

(NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 74.7%; Score 605.4; DB 12; Length 901;
Best Local Similarity 98.7%; Pred. No. 2.8e-156;
Matches 631; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

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Qy        172 GTGTCGGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTG 231
              | |||||||||||||||||||| ||| ||||||||||||||||||||||||||||||||
Db          4 GGGTCGGTCTCCAAGATGGCGGACGCTTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTG 63

Qy        232 ACGGCCAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCT 291
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACGG-CAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCT 122

Qy        292 GTTGCCACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAA 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 GTTGCCACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAA 182

Qy        352 TATATTTGTAAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAAC 411
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 TATATTTGTCAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAAC 242

Qy        412 TACACAGCTCATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGC 471
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 TACACAGCTCATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGC 302

Qy        472 AATGAAACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAAT 531
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Db        303 AATGAAACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAAT 362

Qy        532 GTAAATGGCTATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGA 591
              |  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GGTAATGGCTATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGA 422

Qy        592 GCAGATCGATTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGG 651
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Db        423 GCAGATCGATTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGG 482

Qy        652 TTTTGTGGAATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCT 711
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 -TTTGTGGAATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCT 541

Qy        712 TCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATT 771
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 TCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATT 601

Qy        772 ACTAATGAAACATTTAGAAAAACGCAATTATATCCATAA 810
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Db        602 ACTAATGAAACATTTAGAAAAACGCAATTATATCCATAA 640
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RESULT 14
BI596662
LOCUS BI596662 908 bp mRNA linear EST 07-SEP-2001
DEFINITION 603243232F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5285982 5',

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            mRNA sequence.
ACCESSION   BI596662
VERSION     BI596662.1  GI:15489601
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 908)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11722  row: o  column: 07
            High quality sequence stop: 755.
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                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_96"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
                     (gtcgag); Oligo-dT primed using primer
                     5'-TTTTTTTTTTTTTTTVN-3', size-selected for  average
                     insert size 2.3 kb and normalized to ROT 5. This is a
                     primary library enriched for full-length  clones and
                     constructed using the Cap-trapper method (Carninci, in
                     preparation).  Library constructed by M. Brownstein
                     (NIMH/NHGRI, National Institutes of Health). Note: this is
                     a NIH_MGC Library."
ORIGIN

  Query Match             74.6%;  Score 604.4;  DB 12;  Length 908;
  Best Local Similarity   98.6%;  Pred. No. 5.3e-156;
  Matches  631;  Conservative    0;  Mismatches    6;  Indels    3;  Gaps    2;

Qy        172 GTGTCGGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTG 231
              | |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db          4 GGGTCGGTCTCCAAGATGGCGGCCGCTTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTG 63

Qy        232 ACGGCCAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCT 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ACGGCCAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCT 123
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Qy        292 GTTGCCACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAA 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 GTTGCCACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAA 183

Qy        352 TATATTTGTAAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAAC 411
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 TATATTTGTAAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAAC 243

Qy        412 TACACAGCTCATGTTTCCTGTTTTCCAGCACCCAACATAACTT-GTAAGGATTCCAGTGG 470
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        244 TACACAGCTCATGTTTCCTGTTTTCCAGCACCCAACATAACTTGGTAAGGATTCCAGTGG 303

Qy        471 CAATGAAACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAA 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 CAATGAAACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAA 363

Qy        531 TGTAAATGGCTATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGG 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TGTAAATGGCTATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGG 423

Qy        591 AGCAGATCGATTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGG 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 AGCAGATCGATTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGG 483

Qy        651 GTTTTGTGGAATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACC 710
              ||||    | | ||||||||||||||||||||||||||||||||||||||||||||||
Db        484 GTTT--GTGGAATGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACC 541

Qy        711 TTCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTAT 770
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Db        542 TTCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTAT 601

Qy        771 TACTAATGAAACATTTAGAAAAACGCAATTATATCCATAA 810
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Db        602 TACTAATGAAACATTTAGAAAAACGCAATTATATCCATAA 641
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RESULT 15
AI923178

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LOCUS       AI923178                599 bp    mRNA    linear   EST 02-SEP-1999
DEFINITION  wn67b10.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2450491 3'
            similar to WP:C02F5.3 CE00039 GTP-BINDING PROTEIN ;, mRNA sequence.
ACCESSION   AI923178
VERSION     AI923178.1  GI:5659142
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 599)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
```

Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 457.

FEATURES Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2450491"
/tissue_type="squamous cell carcinoma, poorly differentiated (4 pooled tumors, including primary and metastatic)"
/dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NCI_CGAP_Lu19"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled lung tumor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went througb one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 73.5%; Score 595.4; DB 9; Length 599;
Best Local Similarity 99.5%; Pred. No. 1.4e-153;
Matches 596; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy        190 GCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGCCAGACTCGTTGGT 249
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Db          1 GCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGCCAGACTCGTTGGT 60

Qy        250 GTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCTGTTGCCACCTCCGCCGGG 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCTGTTGCCACCTCCGCCGGG 120

Qy        310 GGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCA 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCA 180

Qy        370 AAAATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCC 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCC 240

Qy        430 TGTTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACT 489
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGTTTTCCAGCACCCCACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACT 300

Qy        490 GGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTAC 549
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTAC 360

Qy        550 AAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTT 609
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Db        361 AAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTT 420

Qy        610 GGATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGC 669
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Db        421 GGATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTANGGTTTTGTGGAATTGGGAGC 480

Qy        670 CTAATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTAC 729
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTAATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTAC 540

Qy        730 ATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAG 788
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        541 ATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATNTAG 599
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Search completed: March 4, 2004, 09:16:38
Job time : 2551 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 05:35:01 ; Search time 3285 Seconds
(without alignments)
10687.323 Million cell updates/sec

Title: US-09-852-100B-1
Perfect score: 810
Sequence: 1 atgcatattttaaaagggtc.....aaacgcaattatatccataa 810

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
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22: em_ov:*
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25: em_pl:*
26: em_ro:*
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30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	810	100.0	810	6	BD243134	BD243134 6-Protein
	2	810	100.0	1246	9	AF353990	AF353990 Homo sapi
	3	645	79.6	984	9	BC029486	BC029486 Homo sapi
	4	602.8	74.4	970	6	BD139411	BD139411 Extended
	5	499	61.6	508	6	BD265227	BD265227 Compounds
	6	499	61.6	508	6	BD265239	BD265239 Compounds
	7	499	61.6	508	6	AR401213	AR401213 Sequence
	8	499	61.6	508	6	AR401225	AR401225 Sequence
	9	499	61.6	508	6	AX192666	AX192666 Sequence
	10	499	61.6	508	6	AX192678	AX192678 Sequence
	11	471.6	58.2	630	10	AF353993	AF353993 Mus muscu
	12	436.8	53.9	440	6	BD076181	BD076181 5' EST of
c	13	430.6	53.2	193660	2	AC102262	AC102262 Mus muscu
	14	425.2	52.5	455	6	BD076249	BD076249 5' EST of
	15	411.4	50.8	487	6	AX892343	AX892343 Sequence
	16	411.4	50.8	487	6	BD027876	BD027876 Sequence
c	17	354	43.7	183425	9	AC097064	AC097064 Homo sapi
c	18	354	43.7	239704	9	AC099791	AC099791 Homo sapi
c	19	325.4	40.2	228458	2	AC097670	AC097670 Rattus no
	20	299	36.9	176056	10	AC073437	AC073437 Mus muscu
	21	299	36.9	196421	10	AL672100	AL672100 Mouse DNA
	22	276	34.1	185576	2	AC025691	AC025691 Homo sapi
c	23	250.4	30.9	231150	2	AC114195	AC114195 Rattus no
	24	244.4	30.2	157999	2	AC117088	AC117088 Rattus no
	25	209.8	25.9	277191	2	AC109077	AC109077 Rattus no
	26	186.2	23.0	167627	9	AC079382	AC079382 Homo sapi
	27	145.6	18.0	178068	2	AC142046	AC142046 Rattus no
c	28	114	14.1	129705	2	AC133258	AC133258 Rattus no
	29	114	14.1	239113	2	AC094034	AC094034 Rattus no
	30	114	14.1	324462	2	AC137263	AC137263 Rattus no
c	31	107.6	13.3	145871	2	AC143611	AC143611 Macaca mu
	32	99.8	12.3	298	6	E25986	E25986 Blastocyst
	33	99.2	12.2	240950	2	AC098287	AC098287 Rattus no

c	34	97.8	12.1	131215	10	AL671140	AL671140 Mouse DNA
c	35	73.2	9.0	198395	2	AC101700	AC101700 Mus muscu
	36	64.6	8.0	128444	2	AC019924	AC019924 Drosophil
	37	64.6	8.0	132637	2	AC006092	AC006092 Drosophil
c	38	64.6	8.0	149592	2	AC005718	AC005718 Drosophil
c	39	64.6	8.0	179139	3	AC099307	AC099307 Drosophil
c	40	64.6	8.0	188633	3	AC007175	AC007175 Drosophil
c	41	64.6	8.0	305150	3	AE003453	AE003453 Drosophil
	42	64.4	8.0	1052	3	AY061343	AY061343 Drosophil
	43	58.2	7.2	155623	5	AL929239	AL929239 Zebrafish
	44	58.2	7.2	239459	2	BX322568	BX322568 Danio rer
c	45	54.6	6.7	214455	2	AC118451	AC118451 Rattus no

ALIGNMENTS

RESULT 1
BD243134
LOCUS BD243134 810 bp DNA linear PAT 17-JUL-2003
DEFINITION 6-Protein-bound receptor-like protein, polynucleotide encoded by it, and method of use thereof.
ACCESSION BD243134
VERSION BD243134.1 GI:33052904
KEYWORDS JP 2002527064-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 810)
AUTHORS Ozenberger,B.A., Kajkowski,E.M. and Lo,C.H.F.
TITLE 6-Protein-bound receptor-like protein, polynucleotide encoded by it, and method of use thereof
JOURNAL Patent: JP 2002527064-A 1 27-AUG-2002;
AMERICAN HOME PRODUCTS CORP
COMMENT OS Homo sapiens (human)
PN JP 2002527064-A/1
PD 27-AUG-2002
PF 13-OCT-1999 JP 2000576015
PR 13-OCT-1998 US 60/104104
PI BRADLEY ALTON OZENBERGER,EILEEN MARIE KAJKOWSKI,CHING HSIUNG
PI FREDERICK LO
PC C12N15/09,A61K45/00,A61P43/00,C07K14/705,C12N1/15,C12N1/19, PC C12N1/21,
PC C12N5/10,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/53, PC G01N33/566,
PC C12N15/00,C12N5/00
CC 6-Protein-bound receptor-like protein, polynucleotide encoded
CC by it, and
CC method of use thereof
FH Key Location/Qualifiers
FT source 1. .810
FT /organism='Homo sapiens (human)'.
FEATURES Location/Qualifiers
source 1. .810
/organism="Homo sapiens"
/mol_type="genomic DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 810; DB 6; Length 810;
Best Local Similarity 100.0%; Pred. No. 2.2e-206;
Matches 810; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        181 TCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGCCAGA 240
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Qy        541 TATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGA 600
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Qy        601 TTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGA 660
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Qy        661 ATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGA 720
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Qy        721 AGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAA 780
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Db        721 AGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAA 780

Qy        781 ACATTTAGAAAAACGCAATTATATCCATAA 810
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Db        781 ACATTTAGAAAAACGCAATTATATCCATAA 810


RESULT 2
AF353990
LOCUS       AF353990                1246 bp    mRNA    linear   PRI 29-MAY-2001
DEFINITION  Homo sapiens beta-amyloid binding protein precursor (BBP) mRNA,
            complete cds.
ACCESSION   AF353990
VERSION     AF353990.1  GI:13625458
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1246)
  AUTHORS   Kajkowski,E.M., Lo,C.F., Ning,X., Walker,S., Sofia,H.J., Wang,W.,
            Edris,W., Chanda,P., Wagner,E., Vile,S., Ryan,K.,
            McHendry-Rinde,B., Smith,S.C., Wood,A., Rhodes,K.J., Kennedy,J.D.,
            Bard,J., Jacobsen,J.S. and Ozenberger,B.A.
  TITLE     beta -Amyloid peptide-induced apoptosis regulated by a novel
            protein containing a g protein activation module
  JOURNAL   J. Biol. Chem. 276 (22), 18748-18756 (2001)
  MEDLINE   21276355
   PUBMED   11278849
REFERENCE   2  (bases 1 to 1246)
  AUTHORS   Ozenberger,B.A., Kajkowski,E., Jacobsen,J.S., Bard,J. and Walker,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-FEB-2001) Wyeth Neuroscience, CN 8000, Princeton, NJ
            08543, USA
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     CDS             304. .927
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ORIGIN

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  Matches  810;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATATTTTAAAAGGGTCTCCCAATGTGATTCCACGGGCTCACGGGCAGAAGAACACG 60
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Db        118 ATGCATATTTTAAAAGGGTCTCCCAATGTGATTCCACGGGCTCACGGGCAGAAGAACACG 177

Qy         61 CGAAGAGACGGAACTGGCCTCTATCCTATGCGAGGTCCCTTTAAGAACCTCGCCCTGTTG 120
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Db        178 CGAAGAGACGGAACTGGCCTCTATCCTATGCGAGGTCCCTTTAAGAACCTCGCCCTGTTG 237

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Qy        181 TCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGCCAGA 240
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Qy        541 TATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGA 600
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Qy        601 TTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGA 660
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Qy        721 AGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAA 780
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RESULT 3
BC029486

LOCUS BC029486 984 bp mRNA linear PRI 06-OCT-2003

DEFINITION Homo sapiens beta-amyloid binding protein precursor, mRNA (cDNA clone MGC:32941 IMAGE:5271098), complete cds.

ACCESSION BC029486

VERSION BC029486.1 GI:20809565

KEYWORDS MGC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 984)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE 22388257

PUBMED 12477932

REFERENCE 2 (bases 1 to 984)

AUTHORS Strausberg,R.

TITLE Direct Submission

JOURNAL Submitted (01-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov

COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 48 Row: b Column: 24
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 17738309.

FEATURES Location/Qualifiers

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ORIGIN

Query Match 79.6%; Score 645; DB 9; Length 984;
Best Local Similarity 100.0%; Pred. No. 4.8e-162;
Matches 645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        286 GGGGCTGTTGCCACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTG 345
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Db        121 GGGGCTGTTGCCACCTCCGCCGGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTG 180

Qy        346 GGACAATATATTTGTAAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAACTGT 405
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Qy        406 ACAAACTACACAGCTCATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGGATTCC 465
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Qy        466 AGTGGCAATGAAACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTGC 525
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Qy        586 TTGGGAGCAGATCGATTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACT 645
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RESULT 4
BD139411
LOCUS       BD139411                970 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Extended cDNA of secretory protein.
ACCESSION   BD139411
VERSION     BD139411.1  GI:23234356
KEYWORDS    JP 2002508182-A/163.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 970)
  AUTHORS   Bougueleret,L., Duclert,A. and Edwards,J.B.D.M.
  TITLE     Extended cDNA of secretory protein
  JOURNAL   Patent: JP 2002508182-A 163 19-MAR-2002;
            GENSET
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002508182-A/163
            PD   19-MAR-2002
            PF   17-DEC-1998 JP 2000539136
            PR   17-DEC-1997 US    60/069957,09-FEB-1998 US    60/074121 PR
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13-APR-1998 US 60/081563,10-AUG-1998 US 60/096116 PI LYDIE
BOUGUELERET,AYMERIC DUCLERT,JEAN BAPTISTE DUMAS MILNE PI EDWARDS
PC C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19, PC
C12N1/21,
PC C12N5/10,C12P21/02,C12Q1/68,C12N15/00,C12N5/00,C12N15/00 CC
Von Heijne matrix
CC score 5.5
CC seq LVGVLWFVSVTTG/PW
FH Key Location/Qualifiers
FT CDS 12. .497
FT sig_peptide 12. .104
FT polyA_signal 935. .940
FT polyA_site 955. .967.

FEATURES Location/Qualifiers
source 1. .970
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 74.4%; Score 602.8; DB 6; Length 970;
Best Local Similarity 98.4%; Pred. No. 1e-150;
Matches 624; Conservative 5; Mismatches 3; Indels 2; Gaps 2;

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Qy        177 GGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGC 236
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Db          2 GGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGKCTGCTCCGGAGGCCGTGACGGC 61

Qy        237 CAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCTGTTGC 296
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Db         62 CAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCTGTTGC 121

Qy        297 CACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATAT 356
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Db        122 CACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATAT 181

Qy        357 TTGTAAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACAC 416
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Db        182 TTGTAAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACAC 241

Qy        417 AGCTCATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGA 476
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Db        242 AGCTCATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGA 301

Qy        477 AACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAA 536
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Db        302 AACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAA 361

Qy        537 TGGCTATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGA 596
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Db        362 TGGCTATTCCTACAATG-AGCAGTCGCA-TGTCTCTTTTTCTTGGATGGTTGGGAGCAGA 419

Qy        597 TCGATTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTG 656
              ||||||||||||||||||||||||||||||||||||:|||:|||||||||||||||:|
Db        420 TCGATTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAABTTTYGCACTGTAGGGTTTKG 479

Qy        657 TGGAATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGA 716
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Db        480 TGGAATTGGGAGCCTAATTGATTTCATYCTTATTTCAATGCAGATTGTTGGACCTTCAAA 539

Qy        717 TGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAA 776
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Db        540 TGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAA 599

Qy        777 TGAAACATTTAGAAAAACGCAATTATATCCATAA 810
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RESULT 5
BD265227
LOCUS       BD265227                 508 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Compounds for immunotherapy and diagnosis of colonic cancer and
            method of using the same.
ACCESSION   BD265227
VERSION     BD265227.1  GI:33074995
KEYWORDS    JP 2002533082-A/225.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 508)
  AUTHORS   Xu,J., Lodes,M.J., Secrist,H., Benson,D.R., Meagher,M.J., Stolk,J.,
            Wang,T. and Yuqiu,J.
  TITLE     Compounds for immunotherapy and diagnosis of colonic cancer and
            method of using the same
  JOURNAL   Patent: JP 2002533082-A 225 08-OCT-2002;
            CORIXA CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002533082-A/225
            PD   08-OCT-2002
            PF   23-DEC-1999 JP 2000589697
            PR   23-DEC-1998 US    09/221298,02-JUL-1999 US    09/347496 PR
            22-SEP-1999 US    09/401064,19-NOV-1999 US    09/444242 PR
            02-DEC-1999 US    09/454150
            PI   JIANGCHUN XU,MICHAEL J LODES,HEATHER SECRIST,DARIN R BENSON,
            PI   MADELEINE JOY MEAGHER,JOHN STOLK,TONGTONG WANG,JIANG YUQIU PC
             C12N15/09,A61K31/711,A61K35/14,A61K38/00,A61K39/00,A61K39/395, PC
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            PC   A61P35/00,C07K14/47,C07K16/18,C07K19/00,C12N1/15,C12N1/19, PC
             C12N1/21,
            PC
            C12N5/06,C12N5/10,C12Q1/02,C12Q1/68,G01N33/53,G01N33/53,G01N33/ PC
             566,
            PC   G01N33/574,G01N33/577,G01N33/58,C12N15/00,C12N5/00,C12N5/00,
            PC   A61K37/02
            CC   Compounds for immunotherapy and diagnosis of colonic cancer
            CC            and method of
            CC   using the same
            FH   Key             Location/Qualifiers
            FT   source          1. .508
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .508
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                     /mol_type="genomic DNA"
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ORIGIN

  Query Match             61.6%;  Score 499;  DB 6;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 6.9e-123;
  Matches  499;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        312 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 371
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Db          1 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 60

Qy        372 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 431
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Db         61 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 120

Qy        432 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 491
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Db        121 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 180

Qy        492 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 551
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Db        181 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 240

Qy        552 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 611
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Db        241 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 300

Qy        612 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 671
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Db        301 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 360

Qy        672 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 731
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Db        361 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 420

Qy        732 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 791
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Db        421 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 480

Qy        792 AACGCAATTATATCCATAA 810
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RESULT 6
BD265239
LOCUS       BD265239                 508 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Compounds for immunotherapy and diagnosis of colonic cancer and
            method of using the same.
ACCESSION   BD265239
VERSION     BD265239.1  GI:33075007
KEYWORDS    JP 2002533082-A/237.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 508)
  AUTHORS   Xu,J., Lodes,M.J., Secrist,H., Benson,D.R., Meagher,M.J., Stolk,J.,
            Wang,T. and Yuqiu,J.
  TITLE     Compounds for immunotherapy and diagnosis of colonic cancer and
            method of using the same
  JOURNAL   Patent: JP 2002533082-A 237 08-OCT-2002;
            CORIXA CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002533082-A/237
            PD   08-OCT-2002
            PF   23-DEC-1999 JP 2000589697
            PR   23-DEC-1998 US    09/221298,02-JUL-1999 US    09/347496 PR
            22-SEP-1999 US    09/401064,19-NOV-1999 US    09/444242 PR
            02-DEC-1999 US    09/454150
            PI   JIANGCHUN XU,MICHAEL J LODES,HEATHER SECRIST,DARIN R BENSON,
            PI   MADELEINE JOY MEAGHER,JOHN STOLK,TONGTONG WANG,JIANG YUQIU PC
             C12N15/09,A61K31/711,A61K35/14,A61K38/00,A61K39/00,A61K39/395, PC
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            PC   A61P35/00,C07K14/47,C07K16/18,C07K19/00,C12N1/15,C12N1/19, PC
             C12N1/21,
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            C12N5/06,C12N5/10,C12Q1/02,C12Q1/68,G01N33/53,G01N33/53,G01N33/ PC
             566,
            PC   G01N33/574,G01N33/577,G01N33/58,C12N15/00,C12N5/00,C12N5/00,
            PC   A61K37/02
            CC   Compounds for immunotherapy and diagnosis of colonic cancer
            CC            and method of
            CC   using the same
            FH   Key             Location/Qualifiers
            FT   source          1. .508
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
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ORIGIN

  Query Match             61.6%;  Score 499;  DB 6;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 6.9e-123;
  Matches  499;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        312 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 371
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Qy        372 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 431
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Db         61 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 120

Qy        432 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 180

Qy        492 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 551
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Db        181 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 240

Qy        552 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 611
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Db        241 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 300

Qy        612 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 671
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Db        301 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 360

Qy        672 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 731
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Db        361 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 420

Qy        732 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 791
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Db        421 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 480

Qy        792 AACGCAATTATATCCATAA 810
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Db        481 AACGCAATTATATCCATAA 499
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RESULT 7
AR401213
LOCUS       AR401213                 508 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 233 from patent US 6623923.
ACCESSION   AR401213
VERSION     AR401213.1  GI:40148513
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 508)
  AUTHORS   Xu,J., Lodes,M.J., Secrist,H., Meagher,M.J., Stolk,J., Benson,D.R.
            and Wang,T.
  TITLE     Compounds for immunotherapy and diagnosis of colon cancer and
            methods for their use
  JOURNAL   Patent: US 6623923-A 233 23-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .508
                     /organism="unknown"
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ORIGIN

  Query Match             61.6%;  Score 499;  DB 6;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 6.9e-123;
  Matches  499;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        312 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 371
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Db          1 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 60

Qy        372 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 431
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Db         61 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 120
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Qy        432 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 491
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Db        121 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 180

Qy        492 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 551
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Db        181 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 240

Qy        552 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 611
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Db        241 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 300

Qy        612 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 671
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Db        301 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 360

Qy        672 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 731
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Qy        732 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 791
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Db        421 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 480

Qy        792 AACGCAATTATATCCATAA 810
              ||||||||||||||||||
Db        481 AACGCAATTATATCCATAA 499


RESULT 8
AR401225
LOCUS       AR401225                 508 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 245 from patent US 6623923.
ACCESSION   AR401225
VERSION     AR401225.1  GI:40148525
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 508)
  AUTHORS   Xu,J., Lodes,M.J., Secrist,H., Meagher,M.J., Stolk,J., Benson,D.R.
            and Wang,T.
  TITLE     Compounds for immunotherapy and diagnosis of colon cancer and
            methods for their use
  JOURNAL   Patent: US 6623923-A 245 23-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .508
                     /organism="unknown"
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ORIGIN

  Query Match             61.6%;  Score 499;  DB 6;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 6.9e-123;
  Matches  499;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        312 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 371
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Db          1 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 60

Qy        372 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 431
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Db         61 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 120

Qy        432 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 180

Qy        492 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 240

Qy        552 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 611
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Db        241 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 300

Qy        612 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 360

Qy        672 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 731
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Db        361 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 420

Qy        732 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 791
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 480

Qy        792 AACGCAATTATATCCATAA 810
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Db        481 AACGCAATTATATCCATAA 499
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RESULT 9
AX192666
LOCUS       AX192666                508 bp    DNA     linear   PAT 15-AUG-2001
DEFINITION  Sequence 233 from Patent WO0149716.
ACCESSION   AX192666
VERSION     AX192666.1  GI:15210622
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Xu,J., Lodes,M.J., Secrist,H., Benson,D.R., Meagher,M.J.,
            Stolk,J.A., King,G.E., Wang,T. and Jiang,Y.
  TITLE     Compounds for immunotherapy and diagnosis of colon cancer and
            methods for their use
  JOURNAL   Patent: WO 0149716-A 233 12-JUL-2001;
            CORIXA CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .508
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
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/db_xref="taxon:9606"

ORIGIN

Query Match 61.6%; Score 499; DB 6; Length 508;
Best Local Similarity 100.0%; Pred. No. 6.9e-123;
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        312 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 60

Qy        372 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 120

Qy        432 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 180

Qy        492 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 240

Qy        552 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 611
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 300

Qy        612 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 360

Qy        672 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 731
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 420

Qy        732 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 791
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 480

Qy        792 AACGCAATTATATCCATAA 810
              ||||||||||||||||||
Db        481 AACGCAATTATATCCATAA 499
```

RESULT 10
AX192678

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LOCUS       AX192678                 508 bp    DNA     linear   PAT 15-AUG-2001
DEFINITION  Sequence 245 from Patent WO0149716.
ACCESSION   AX192678
VERSION     AX192678.1  GI:15210634
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Xu,J., Lodes,M.J., Secrist,H., Benson,D.R., Meagher,M.J.,
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            Stolk,J.A., King,G.E., Wang,T. and Jiang,Y.
  TITLE     Compounds for immunotherapy and diagnosis of colon cancer and
            methods for their use
  JOURNAL   Patent: WO 0149716-A 245 12-JUL-2001;
            CORIXA CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .508
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             61.6%;  Score 499;  DB 6;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 6.9e-123;
  Matches  499;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        312 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 60

Qy        372 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 120

Qy        432 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 180

Qy        492 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 240

Qy        552 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 611
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Db        241 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 300

Qy        612 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 360

Qy        672 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 731
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 420

Qy        732 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 791
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 480

Qy        792 AACGCAATTATATCCATAA 810
              ||||||||||||||||||
Db        481 AACGCAATTATATCCATAA 499


RESULT 11
AF353993
LOCUS       AF353993                630 bp    mRNA    linear   ROD 29-MAY-2001
DEFINITION  Mus musculus beta-amyloid binding protein (Bbp) mRNA, complete cds.
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ACCESSION   AF353993
VERSION     AF353993.1  GI:13625464
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 630)
  AUTHORS   Kajkowski,E.M., Lo,C.F., Ning,X., Walker,S., Sofia,H.J., Wang,W.,
            Edris,W., Chanda,P., Wagner,E., Vile,S., Ryan,K.,
            McHendry-Rinde,B., Smith,S.C., Wood,A., Rhodes,K.J., Kennedy,J.D.,
            Bard,J., Jacobsen,J.S. and Ozenberger,B.A.
  TITLE     beta -Amyloid peptide-induced apoptosis regulated by a novel
            protein containing a g protein activation module
  JOURNAL   J. Biol. Chem. 276 (22), 18748-18756 (2001)
  MEDLINE   21276355
   PUBMED   11278849
REFERENCE   2  (bases 1 to 630)
  AUTHORS   Ozenberger,B.A., Howland,D.S., Lo,C.F. and She,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-FEB-2001) Wyeth Neuroscience, CN 8000, Princeton, NJ
            08543, USA
FEATURES             Location/Qualifiers
     source          1. .630
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="BALB/c"
                     /db_xref="taxon:10090"
     gene            1. .630
                     /gene="Bbp"
     CDS             4. .630
                     /gene="Bbp"
                     /note="integral membrane glycoprotein"
                     /codon_start=1
                     /product="beta-amyloid binding protein"
                     /protein_id="AAK35067.1"
                     /db_xref="GI:13625465"
                     /translation="MAAAWPAGRASPAAGPPGLLRTLWLVTVAAGHCGAAASGAVGGE
                     ETPKCEDLRVGQYICKEPKINDATQEPVNCTNYTAHVQCFPAPKITCKDLSGNETHFT
                     GSEVGFLKPISCRNVNGYSYKVAVALSLFLGWLGADRFYLGYPALGLLKFCTVGFCGI
                     GSLIDFILISMQIVGPSDGSSYIIDYYGTRLTRLSITNETFRKTQLYP"
     misc_feature    349. .414
                     /gene="Bbp"
                     /note="Region: transmembrane domain"
     misc_feature    457. .528
                     /gene="Bbp"
                     /note="Region: transmembrane domain"
ORIGIN
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Query Match 58.2%; Score 471.6; DB 10; Length 630;
Best Local Similarity 85.4%; Pred. No. 1.6e-115;
Matches 538; Conservative 0; Mismatches 89; Indels 3; Gaps 1;

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Qy        184 AAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGCCAGACTC 243
              || ||||||||||||||||  | |||| | || | || | ||| | | |  |  | ||
Db          1 AACATGGCGGCCGCCTGGCCCGCGGGTCGGGCTTCCCCAGCGGCGGGGCCTCCGGGCCTT 60
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```
Qy        244 GTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCTGTTGCCAC---C 300
              |  |   ||||||| ||||  | ||| |  | |||| ||| ||||||| |||| |   |
Db         61 CTCCGCACCCTGTGGCTCGTGACGGTCGCCGCGGGACACTGTGGGGCTGCTGCCTCTGGC 120

Qy        301 TCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGT 360
              | | |||||||||||||| | |  ||||| |||||||||| ||||||||||||||||||
Db        121 GCTGTCGGGGGCGAGGAGACACCCAAGTGTGAGGACCTCAGGGTGGGACAATATATTTGT 180

Qy        361 AAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCT 420
              |||||  |||||||||||||| |||||||||||||||||| ||||||||||||||||||
Db        181 AAAGAACCAAAAATAAATGATGCTACGCAAGAACCAGTTAATTGTACAAACTACACAGCT 240

Qy        421 CATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACA 480
              ||||||   |||||||||||||||| |||||||||||||||  ||||| |||||||||
Db        241 CATGTTCAATGTTTTCCAGCACCCAAAATAACTTGTAAGGATTTGAGTGGTAATGAAACA 300

Qy        481 CATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGC 540
              |||||||||||  |  ||||| |||||| |||||||||||||||||||||||||| ||||||
Db        301 CATTTTACTGGAAGTGAAGTCGGTTTTCTCAAGCCCATATCTTGCCGAAATGTGAATGGC 360

Qy        541 TATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGA 600
              |||||  |||||||||||||| |||||  |||||  ||| | ||||||  ||||||||||||||
Db        361 TATTCGTACAAAGTGGCAGTTGCATTATCTCTCTTTTTGGGATGGCTGGGAGCAGATCGA 420

Qy        601 TTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGA 660
              ||||||||  |||||  |||||  ||  ||  ||||||||  ||||||||  |||||  |||||  |||
Db        421 TTTTACCTCGGATATCCTGCCTTAGGCTTGTTAAAATTTTGCACCGTAGGATTTTGCGGA 480

Qy        661 ATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGA 540

Qy        721 AGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAA 780
              ||||||||||||||||  ||  ||||||||||  ||||||||||  ||  ||||||||||||
Db        541 AGTAGTTACATTATAGACTATTATGGAACCAGGCTTACAAGACTCAGCATTACTAATGAA 600

Qy        781 ACATTTAGAAAAACGCAATTATATCCATAA 810
              |||||||||||||| ||  | || ||||||
Db        601 ACATTTAGAAAAACCCAGCTGTACCCATAA 630
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RESULT 12
BD076181

LOCUS	BD076181	440 bp	DNA	linear	PAT 27-AUG-2002

DEFINITION 5' EST of tissue-nonspecific secretory protein.
ACCESSION BD076181
VERSION BD076181.1 GI:22621784
KEYWORDS JP 2001512011-A/129.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 440)
AUTHORS Edwards,J.B.D.M., Duclert,A. and Lacroix,B.
TITLE 5' EST of tissue-nonspecific secretory protein
JOURNAL Patent: JP 2001512011-A 129 21-AUG-2001;
GENSET

COMMENT OS Homo sapiens (human)
PN JP 2001512011-A/129
PD 21-AUG-2001
PF 31-JUL-1998 JP 2000505289
PR 01-AUG-1997 US 08/905135
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,AYMERIC DUCLERT,BRUNO PI
LACROIX
PC C12N15/09,C12N15/09,C07K14/47,C12Q1/68,C12N15/00,C12N15/00 CC
blastn
CC identity 97
CC region 113. .315
CC id AA143062
CC est
CC blastn
CC identity 99
CC region 304. .411
CC id AA143062
CC est
CC blastn
CC identity 97
CC region 43. .120
CC id AA143062
CC est
CC blastn
CC identity 97
CC region 44. .317
CC id HUM172D06B
CC est
CC blastn
CC identity 100
CC region 340. .410
CC id HUM172D06B
CC est
CC blastn
CC identity 94
CC region 8. .46
CC id HUM172D06B
CC est
CC blastn
CC identity 100
CC region 125. .414
CC id N47594
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            CC   est
            CC   blastn
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            FT   misc_feature    143. .345
            FT   misc_feature    335. .442
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            FT   misc_feature    72. .345
            FT   misc_feature    372. .442
            FT   misc_feature    35. .73
            FT   misc_feature    153. .442
            FT   misc_feature    77. .147
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            FT   misc_feature    27. .73
            FT   misc_feature    143. .367
            FT   misc_feature    80. .147
            FT   misc_feature    362. .429
            FT   sig_peptide     24. .431.
FEATURES             Location/Qualifiers
     source          1. .440
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             53.9%;  Score 436.8;  DB 6;  Length 440;
  Best Local Similarity   99.5%;  Pred. No. 3.4e-106;
  Matches  436;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        166 GAGAAAGTGTCGGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGAG 225
              ||||||||||||||||||||||||||||||||||||||||::|||||||||||||||||||
Db          3 GAGAAAGTGTCGGTCTCCAAGATGGCGGCCGCCTGGCSDTCTGGTCCGTCTGCTCCGGAG 62

Qy        226 GCCGTGACGGCCAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGG 285
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 GCCGTGACGGCCAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGG 122

Qy        286 GGGGCTGTTGCCACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTG 345
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 GGGGCTGTTGCCACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTG 182
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Qy        346 GGACAATATATTTGTAAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAACTGT 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 GGACAATATATTTGTAAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAACTGT 242

Qy        406 ACAAACTACACAGCTCATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGGATTCC 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 ACAAACTACACAGCTCATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGGATTCC 302

Qy        466 AGTGGCAATGAAACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTGC 525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 AGTGGCAATGAAACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTGC 362

Qy        526 CGAAATGTAAATGGCTATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGG 585
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 CGAAATGTAAATGGCTATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGG 422

Qy        586 TTGGGAGCAGATCGATTT 603
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Db        423 TTGGGAGCAGATCGATTT 440
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RESULT 13
AC102262/c

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LOCUS       AC102262               193660 bp    DNA     linear   HTG 27-FEB-2003
DEFINITION  Mus musculus clone RP24-216B4, WORKING DRAFT SEQUENCE, 9 unordered
            pieces.
ACCESSION   AC102262
VERSION     AC102262.3  GI:28570462
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 193660)
  AUTHORS   Birren,B., Nusbaum,C. and Lander,E.
  TITLE     Mus musculus, clone RP24-216B4
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 193660)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
            Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B.,
            Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
            Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
            Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
            Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
            Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
            Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
            Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
            Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Liu,G.,
            MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
            McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,
            Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
            Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
            Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
            Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
            Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
            Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
            Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
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Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE Direct Submission

JOURNAL Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE 3 (bases 1 to 193660)

AUTHORS Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C., Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE Direct Submission

JOURNAL Submitted (27-FEB-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT On Feb 27, 2003 this sequence version replaced gi:22381123.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
-------------- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
-------------- Project Information
Center project name: L18275
Center clone name: 216_B_4
-------------- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 191505 bases at least Q40
Consensus quality: 192178 bases at least Q30
Consensus quality: 192605 bases at least Q20
Insert size: 188000; agarose-fp
Insert size: 192860; sum-of-contigs
Quality coverage: 10.3 in Q20 bases; agarose-fp
Quality coverage: 10.0 in Q20 bases; sum-of-contigs
--------------.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is

```
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1    16245: contig of 16245 bp in length
            *    16246    16345: gap of 100 bp
            *    16346    17545: contig of 1200 bp in length
            *    17546    17645: gap of 100 bp
            *    17646    21998: contig of 4353 bp in length
            *    21999    22098: gap of 100 bp
            *    22099    31133: contig of 9035 bp in length
            *    31134    31233: gap of 100 bp
            *    31234    41801: contig of 10568 bp in length
            *    41802    41901: gap of 100 bp
            *    41902    62223: contig of 20322 bp in length
            *    62224    62323: gap of 100 bp
            *    62324    91590: contig of 29267 bp in length
            *    91591    91690: gap of 100 bp
            *    91691   123816: contig of 32126 bp in length
            *   123817   123916: gap of 100 bp
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FEATURES             Location/Qualifiers
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     misc_feature    22099. .31133
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     misc_feature    31234. .41801
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     misc_feature    41902. .62223
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     misc_feature    123917. .193660
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                     vector_side:right"
ORIGIN

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  Best Local Similarity   81.7%;  Pred. No. 5.2e-104;
  Matches  535;  Conservative    0;  Mismatches  114;  Indels    6;  Gaps    3;
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Qy        159 AAGTGGCGAGAAAGTGTCGGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGC 218
              ||  |||  | | |   | ||  |||| |||||||| ||||||||  | || | | || |
Db     138927 AAAAGGCTGGGAGGACGCAGTGCCCAACATGGCGGCTGCCTGGCCCGCGGGCCGGGCTTC
138868

Qy        219 TCCGGAGGCCGTGACGGCCAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGG 278
               || |  |||| | |  |  | ||  |  |    |||||| ||||    |||||    ||
Db     138867 CCCAGCAGCCGGGCCTCCGGGCCTTCTCCGCACTCTGTGGCTCGTGATGGTCACCGAGGG
138808

Qy        279 ACCCTGGGGGGCTGTTGCCACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCT 338
              || ||| ||||||| |||| |   ||| |  || |  |||  |   | ||| ||||||||
Db     138807 ACACTGTGGGGCTGCTGCCTCTGGCGCTGTCGGGGGCGAGGAG---AGGTGTGAGGACCT
138751

Qy        339 CAAAGTGGGACAATATATTTGT--AAAGATCCAAAAATAAATGACGCTACGCAAGAACCA 396
              ||  |||||||||||||||||  ||||| |||||||||||||| |||||||||||||||
Db     138750 CAGGGTGGGACAATATATTTGTAAAAAGAACCAAAAATAAATGATGCTACGCAAGAACCA
138691

Qy        397 GTTAACTGTACAAACTACACAGCTCATGTTTCCTGTTTTCCAGCACCCAACATAACTTGT 456
              |||||  |||||||||||||||||||||||   |||||||||||||||| ||||||| |
Db     138690 GTTAATTGTACAAACTACACAGCTCATGTTCAATGTTTTCCAGCACCCAAAATAACTTAT
138631

Qy        457 -AAGGATTCCAGTGGCAATGAAACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCC 515
               |||||||  |||||  |||||||||||||||||||  |  |||||  ||||||  |||||||
Db     138630 AAAGGATTTGAGTGGTAATGAAACACATTTTACTGGAAGTGAAGTCGGTTTTCTCAAGCC
138571

Qy        516 CATATCTTGCCGAAATGTAAATGGCTATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTT 575
              ||||  ||||||||||||  ||||||||||  |||||||||||||  |||||  |||||  ||
Db     138570 CATAACTTGCCGAAATGTGAATGGCTATTCGTACAAAGTGGCAGTTGCATTATCTCTCTT
138511

Qy        576 TCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAA 635
              | | ||||||  |||||||||||||||||||||  |||||  |||||  ||   | ||||||||
Db     138510 TTTGGGATGGCTGGGAGCAGATCGATTTTACCTCGGATATCCTGCCTTACGCTTGTTAAA
138451

Qy        636 GTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCTAATTGATTTCATTCTTATTTCAAT 695
               ||||||||  |||||  |||||  ||||||||||||||||||||||||||||||||||||
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138391

Qy        696 GCAGATTGTTGGACCTTCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACT 755
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     138390 GCAGATTGTTGGACCTTCAGATGGAAGTAGTTACATTATAGACTATTATGGAACCAGGCT
138331

Qy        756 TACAAGACTGAGTATTACTAATGAAACATTTAGAAAAACGCAATTATATCCATAA 810
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Db     138330 TACAAGACTCAGCATTACTAATGAAACATTTAGAAAAACCTAGCTGTACCCATAA 138276


RESULT 14
BD076249
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LOCUS BD076249 455 bp DNA linear PAT 27-AUG-2002
DEFINITION 5' EST of tissue-nonspecific secretory protein.
ACCESSION BD076249
VERSION BD076249.1 GI:22621852
KEYWORDS JP 2001512011-A/197.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 455)
AUTHORS Edwards,J.B.D.M., Duclert,A. and Lacroix,B.
TITLE 5' EST of tissue-nonspecific secretory protein
JOURNAL Patent: JP 2001512011-A 197 21-AUG-2001;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2001512011-A/197
PD 21-AUG-2001
PF 31-JUL-1998 JP 2000505289
PR 01-AUG-1997 US 08/905135
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,AYMERIC DUCLERT,BRUNO PI
LACROIX
PC C12N15/09,C12N15/09,C07K14/47,C12Q1/68,C12N15/00,C12N15/00 CC
blastn
CC identity 99
CC region 125. .358
CC id N47594
CC est
CC blastn
CC identity 100
CC region 49. .119
CC id N47594
CC est
CC blastn
CC identity 96
CC region 374. .438
CC id N47594
CC est
CC blastn
CC identity 96
CC region 113. .315
CC id AA143062
CC est
CC blastn
CC identity 97
CC region 43. .120
CC id AA143062
CC est
CC blastn
CC identity 98
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CC id AA143062
CC est
CC blastn
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CC region 371. .416
CC id AA143062
CC est

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CC   blastn
CC   identity 97
CC   region 44. .317
CC   id HUM172D06B
CC   est
CC   blastn
CC   identity 97
CC   region 370. .416
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CC   est
CC   blastn
CC   identity 97
CC   region 8. .46
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CC   est
CC   blastn
CC   identity 97
CC   region 45. .359
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CC   est
CC   blastn
CC   identity 98
CC   region 92. .316
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CC   est
CC   blastn
CC   identity 100
CC   region 30. .97
CC   id N34957
CC   est
CC   Von Heijne matrix
CC   score 5.5
CC   seq LVGVLWFVSVTTG/PW
CC   n=a, g, c or t
FH   Key             Location/Qualifiers
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FT   misc_feature    60. .137
FT   misc_feature    323. .374
FT   misc_feature    388. .433
FT   misc_feature    60. .333
FT   misc_feature    388. .434
FT   misc_feature    23. .61
FT   misc_feature    60. .374
FT   misc_feature    15. .61
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FT   sig_peptide     12. .104
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            FT   misc_feature    385. .387.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
ORIGIN

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Qy        177 GGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGC 236
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Db          2 GGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGKCTGCTCCGGAGGCCGTGACGGC 61

Qy        237 CAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCTGTTGC 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCTGTTGC 121

Qy        297 CACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATAT 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 CACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATAT 181

Qy        357 TTGTAAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACAC 416
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 TTGTAAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACAC 241

Qy        417 AGCTCATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGA 476
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        242 AGCTCATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGGATNCCAGTGGCAATGA 301

Qy        477 AACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAA 536
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Db        302 AACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAA 361

Qy        537 TGGCTATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGA 596
              ||||||||||||    |:         :||||||||||||||||||||||||||||||||
Db        362 TGGCTATTCCTAC--NNTKAGCAGTNNNWTGTCTCTTTTTCTTGGATGGTTGGGAGCAGA 419

Qy        597 TCGATTTTACCTTGGATACCCTGCTTTGGGTTTGTT 632
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Db        420 TCGATTTTACCTTGGATACCCTGCTTTGGGTTTGTT 455


RESULT 15
AX892343
LOCUS       AX892343                 487 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 8206 from Patent EP1033401.
ACCESSION   AX892343
VERSION     AX892343.1  GI:40047227
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
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  AUTHORS   Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
  TITLE     Expressed sequence tags and encoded human proteins
  JOURNAL   Patent: EP 1033401-A 8206 06-SEP-2000;
            Genset (FR)
FEATURES             Location/Qualifiers
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ORIGIN

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  Matches  445;  Conservative    9;  Mismatches   10;  Indels   23;  Gaps    1;

Qy        164 GCGAGAAAGTGTCGGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGG 223
              ||||||||||||||||||||||||||||||||:||| |||||||:||| :||| ||||
Db          1 GCGAGAAAGTGTCGGTCTCCAAGATGGCGGCCGCMTGGACGTCTGGWCCGAMTGCACCGG 60

Qy        224 AGGCCGTGACGGCCAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCT 283
              | ||||||||||||||:||||||||||||||||||:|||:||||||||||||||||
Db         61 AAGCCGTGACGGCCAGAMTCGTTGGTGTCCTGTGGTTCGTMTCARTCACTACAGGACCCT 120

Qy        284 GGGGGGCTGTTGCCACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAG 343
              ||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        121 GGGGGGCTGTTGCCACCTCCGCCGGGGGCRAGGAGTCGCTTAAGTGCGAGGACCTCAAAG 180

Qy        344 TGGGACAATATATT----------------------TGTAAAGATCCAAAAATAAATGA 380
              ||::|||||||  |                      |   ||||||||||||||||||
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Qy        381 CGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTGTTTTCCAGC 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTGTTTTCCAGC 300

Qy        441 ACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGGGAACGAAGT 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGGGAACGAAGT 360

Qy        501 TGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAAAGTGGCAGT 560
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Db        361 TGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAAAGTGGCAGT 420

Qy        561 CGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGGATACCCTGC 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGGATACCCTGC 480

Qy        621 TTTGGGT 627
              |||||||
Db        481 TTTGGGT 487


Search completed: March  4, 2004, 08:34:00
Job time : 3291 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 03:41:27 ; Search time 385 Seconds
(without alignments)
8937.767 Million cell updates/sec

Title: US-09-852-100B-1
Perfect score: 810
Sequence: 1 atgcatattttaaaagggtc.....aaacgcaattatatccataa 810

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	810	100.0	810	2	AAX05735	Aax05735 Human bet
2	810	100.0	810	3	AAZ52369	Aaz52369 Human bet
3	810	100.0	810	7	AAD51940	Aad51940 Human BBP
4	810	100.0	1246	7	AAD51979	Aad51979 Human BBP
5	602.8	74.4	970	2	AAX97705	Aax97705 Extended
6	499	61.6	508	3	AAA77946	Aaa77946 cDNA enco
7	499	61.6	508	3	AAA77958	Aaa77958 cDNA enco
8	499	61.6	508	4	AAI28684	Aai28684 Colon tum

	9	499	61.6	508	4	AAI28696	Aai28696 Colon tum
	10	499	61.6	508	7	ABZ32882	Abz32882 Human col
	11	499	61.6	508	7	ABZ32870	Abz32870 Human col
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	14	425.2	52.5	455	2	AAX41259	Aax41259 Human sec
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	16	337.4	41.7	431	8	ACH19706	Ach19706 Human adu
	17	322	39.8	323	7	ACD92727	Acd92727 Human col
	18	320.4	39.6	323	7	ACD92728	Acd92728 Human col
c	19	182.4	22.5	561	6	ABQ57089	Abq57089 Human col
	20	153.2	18.9	515	9	ADB56631	Adb56631 Toxicity-
	21	115.4	14.2	433	5	ABV17809	Abv17809 Human pro
	22	115.4	14.2	487	5	ABV47601	Abv47601 Human pro
	23	113	14.0	292	7	AAD51978	Aad51978 Human BBP
	24	99.8	12.3	298	2	AAX85735	Aax85735 Novel cDN
c	25	64.6	8.0	2771	4	ABL16838	Abl16838 Drosophil
c	26	64.6	8.0	3642	4	ABL15742	Abl15742 Drosophil
	27	64.4	8.0	706	4	ABL16839	Abl16839 Drosophil
	28	51	6.3	1369	2	AAX85024	Aax85024 Human sec
	29	51	6.3	1369	7	ADA56147	Ada56147 Gene enco
	30	51	6.3	1369	7	ACD18950	Acd18950 Novel hum
	31	51	6.3	1369	7	ACC50529	Acc50529 Human sec
	32	51	6.3	1369	7	ABZ71291	Abz71291 Secreted
	33	51	6.3	1369	8	ADB91205	Adb91205 Human sec
	34	51	6.3	1369	9	ADC73589	Adc73589 Human sec
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	36	50.4	6.2	854	3	AAA64412	Aaa64412 DNA encod
c	37	50.2	6.2	439	6	ABK62922	Abk62922 Rat seque
c	38	50.2	6.2	439	9	ADB56953	Adb56953 Toxicity-
	39	49.8	6.1	741	3	AAA64409	Aaa64409 Open read
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	41	49.8	6.1	1406	7	ACC51100	Acc51100 Human Amy
	42	49.8	6.1	1455	4	AAF80523	Aaf80523 Receptor
	43	49.8	6.1	1473	3	AAA64408	Aaa64408 DNA encod
	44	49.8	6.1	1473	3	AAA64425	Aaa64425 DNA encod
	45	49.8	6.1	1473	3	AAA64424	Aaa64424 DNA encod

ALIGNMENTS

RESULT 1
AAX05735
ID AAX05735 standard; mRNA; 810 BP.
XX
AC AAX05735;
XX
DT 27-APR-1999 (first entry)
XX
DE Human beta-amyloid peptide-binding protein (BBP) encoding mRNA.
XX
KW Beta-amyloid peptide binding protein; BBP; beta-amyloid protein; BAP;
KW human; Alzheimer's disease; ss.
XX
OS Homo sapiens.
XX

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FH   Key             Location/Qualifiers
FT   CDS             1. .810
FT                   /*tag=  a
FT                   /product= "BBP"
XX
PN   WO9846636-A2.
XX
PD   22-OCT-1998.
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PF   14-APR-1998;   98WO-US007462.
XX
PR   16-APR-1997;   97US-0064583P.
XX
PA   (AMHP ) AMERICAN HOME PROD CORP.
XX
PI   Ozenberger BA,  Kajkowski EM,  Jacobsen JS,  Bard JA,  Walker SG;
XX
DR   WPI; 1999-080736/07.
DR   P-PSDB; AAW94291.
XX
PT   Polynucleotide encoding beta-amyloid peptide binding protein - used to
PT   identify inhibitors of beta-amyloid peptide for treating Alzheimer's
PT   disease.
XX
PS   Claim 1; Page 43-44; 59pp; English.
XX
CC   This represents a nucleotide sequence encoding a beta-amyloid peptide
CC   binding protein (BBP). The polynucleotide comprising the entire BBP
CC   nucleotide sequence of clone BBP1-fl is deposited under the accession
CC   number ATCC 98617. The polynucleotide comprising a fragment of BBP
CC   (nucleotides 202-807 of the full length BBP) of clone pEK196 is deposited
CC   as ATCC 98399. Host cells transformed with a vector comprising the BBP
CC   nucleic acid are used for the recombinant production of the protein. The
CC   protein can be used in a method for diagnosing a disease characterised by
CC   aberrant expression of human beta-amyloid protein (BAP). The protein can
CC   also be used in a method for screening for compounds which regulate
CC   expression of a BAP binding protein. The proteins, antibodies and
CC   identified compounds can be used in the treatment or prevention of
CC   Alzheimer's disease
XX
SQ   Sequence 810 BP; 204 A; 183 C; 202 G; 221 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 810;  DB 2;  Length 810;
  Best Local Similarity   100.0%;  Pred. No. 2e-233;
  Matches  810;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATATTTTAAAAGGGTCTCCCAATGTGATTCCACGGGCTCACGGGCAGAAGAACACG 60
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Db          1 ATGCATATTTTAAAAGGGTCTCCCAATGTGATTCCACGGGCTCACGGGCAGAAGAACACG 60

Qy         61 CGAAGAGACGGAACTGGCCTCTATCCTATGCGAGGTCCCTTTAAGAACCTCGCCCTGTTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGAAGAGACGGAACTGGCCTCTATCCTATGCGAGGTCCCTTTAAGAACCTCGCCCTGTTG 120

Qy        121 CCCTTCTCCCTCCCGCTCCTGGGCGGAGGCGGAAGCGGAAGTGGCGAGAAAGTGTCGGTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCTTCTCCCTCCCGCTCCTGGGCGGAGGCGGAAGCGGAAGTGGCGAGAAAGTGTCGGTC 180
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Qy        181 TCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGCCAGA 240
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Db        181 TCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGCCAGA 240

Qy        241 CTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCTGTTGCCACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCTGTTGCCACC 300

Qy        301 TCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGT 360

Qy        361 AAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCT 420

Qy        421 CATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACA 480

Qy        481 CATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGC 540

Qy        541 TATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGA 600

Qy        601 TTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGA 660

Qy        661 ATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGA 720

Qy        721 AGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAA 780

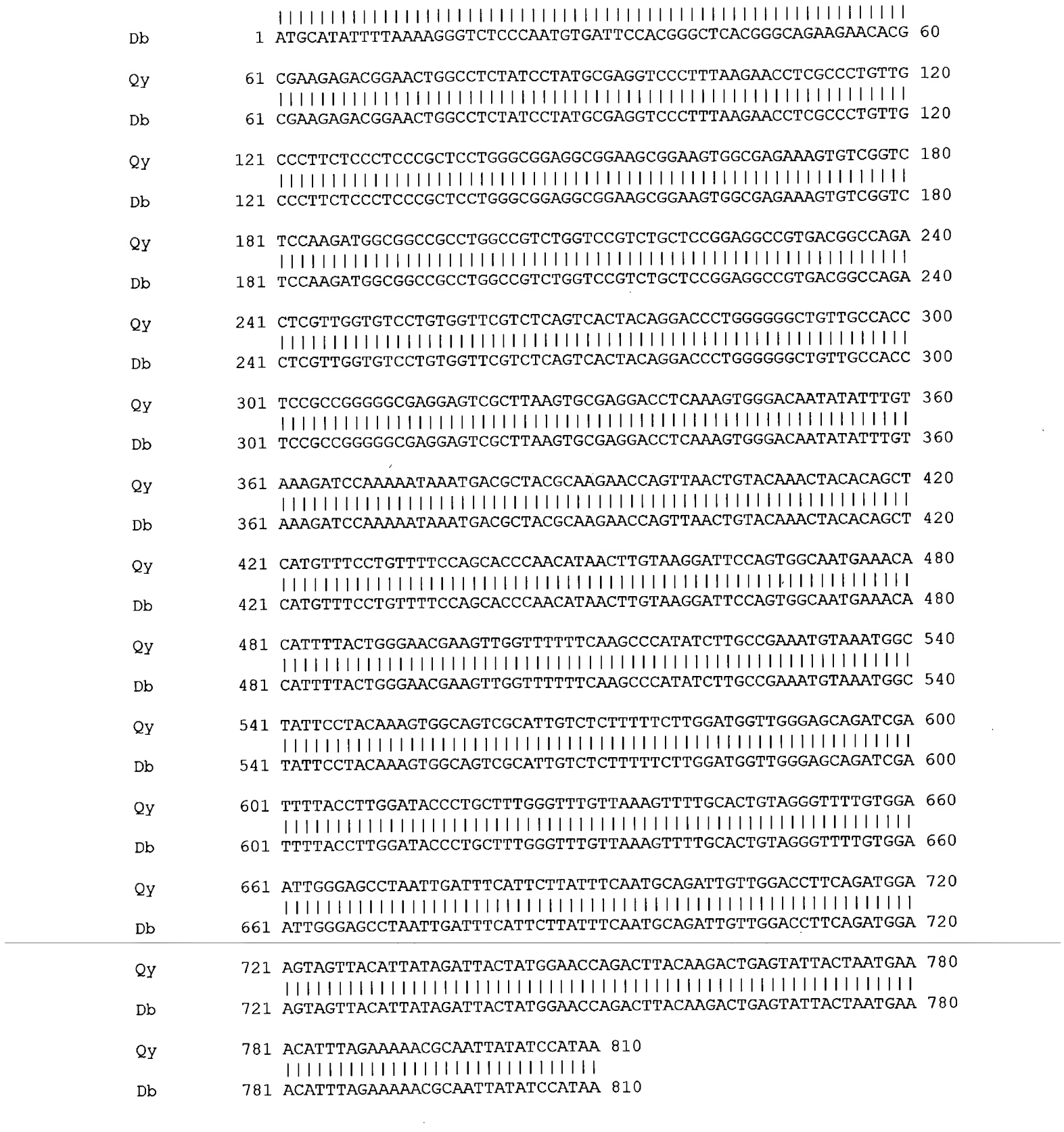
Qy        781 ACATTTAGAAAAACGCAATTATATCCATAA 810
              ||||||||||||||||||||||||||||||
Db        781 ACATTTAGAAAAACGCAATTATATCCATAA 810
```

RESULT 2
AAZ52369
ID AAZ52369 standard; cDNA; 810 BP.
XX
AC AAZ52369;
XX
DT 24-JUL-2000 (first entry)
XX
DE Human beta-amyloid peptide (BAP) binding protein, BBP1 encoding cDNA.
XX
KW Beta-amyloid peptide binding protein; BBP; BAP; tumour; suppressor;

KW G-protein coupled receptor; GPCR; integral membrane protein; antigen;
KW neuronal cell; nonhuman primate; NHP; G-protein signalling pathway;
KW apoptosis; immunogen; therapeutic; treatment; prevention; diagnostic; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1. .810
FT   /*tag= a
FT   /product= "Human BBP1 protein"
FT   /note= "Member of G-protein coupled receptor superfamily"
XX
PN WO200022125-A2.
XX
PD 20-APR-2000.
XX
PF 13-OCT-1999; 99WO-US021621.
XX
PR 13-OCT-1998; 98US-0104104P.
XX
PA (AMHP) AMERICAN HOME PROD CORP.
XX
PI Ozenberger BA, Kajkowski EM, Lo CF;
XX
DR WPI; 2000-317982/27.
DR P-PSDB; AAY70759.
XX
PT Novel G-protein-coupled receptor-like proteins and polynucleotides useful
PT for regulating apoptosis, comprises integral membrane protein traversing
PT the membrane twice.
XX
PS Example 1; Page 60-61; 68pp; English.
XX
CC The present sequence is the cDNA encoding beta-amyloid peptide (BAP)
CC binding protein-1 (BBP1). It is an integral membrane protein, that
CC traverse the membrane twice. It is related to G protein-coupled receptor
CC (GPCR) protein superfamily. It interacts with G-alpha proteins and
CC regulates the activity of G-protein signalling pathways. BBP genes are
CC widely expressed in neuronal cells of nonhuman primate (NHP) brain and
CC overexpressed in some tumours. It functions as a suppressor of apoptosis
CC induction. BBP proteins are used as immunogens to raise antibodies,
CC useful as therapeutics and as antigens in solid phase assays. They are
CC also useful as reagents to identify molecules which effect the
CC interaction of BBP and a cloned protein, that are useful in the treatment
CC or prevention of diseases associated with apoptosis. The polynucleotides
CC are useful for diagnostics. Note: In claim 5, the patent claims an amino
CC acid sequence from figure 2. However, figure 2 does not contain any
CC sequence. It is inferred from the disclosure that the figure 2 sequence
CC refers to BBP1 protein, encoded by this polynucleotide sequence
XX
SQ Sequence 810 BP; 204 A; 183 C; 202 G; 221 T; 0 U; 0 Other;

  Query Match   100.0%; Score 810; DB 3; Length 810;
  Best Local Similarity   100.0%; Pred. No. 2e-233;
  Matches 810; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ATGCATATTTTAAAAGGGTCTCCCAATGTGATTCCACGGGCTCACGGGCAGAAGAACACG 60

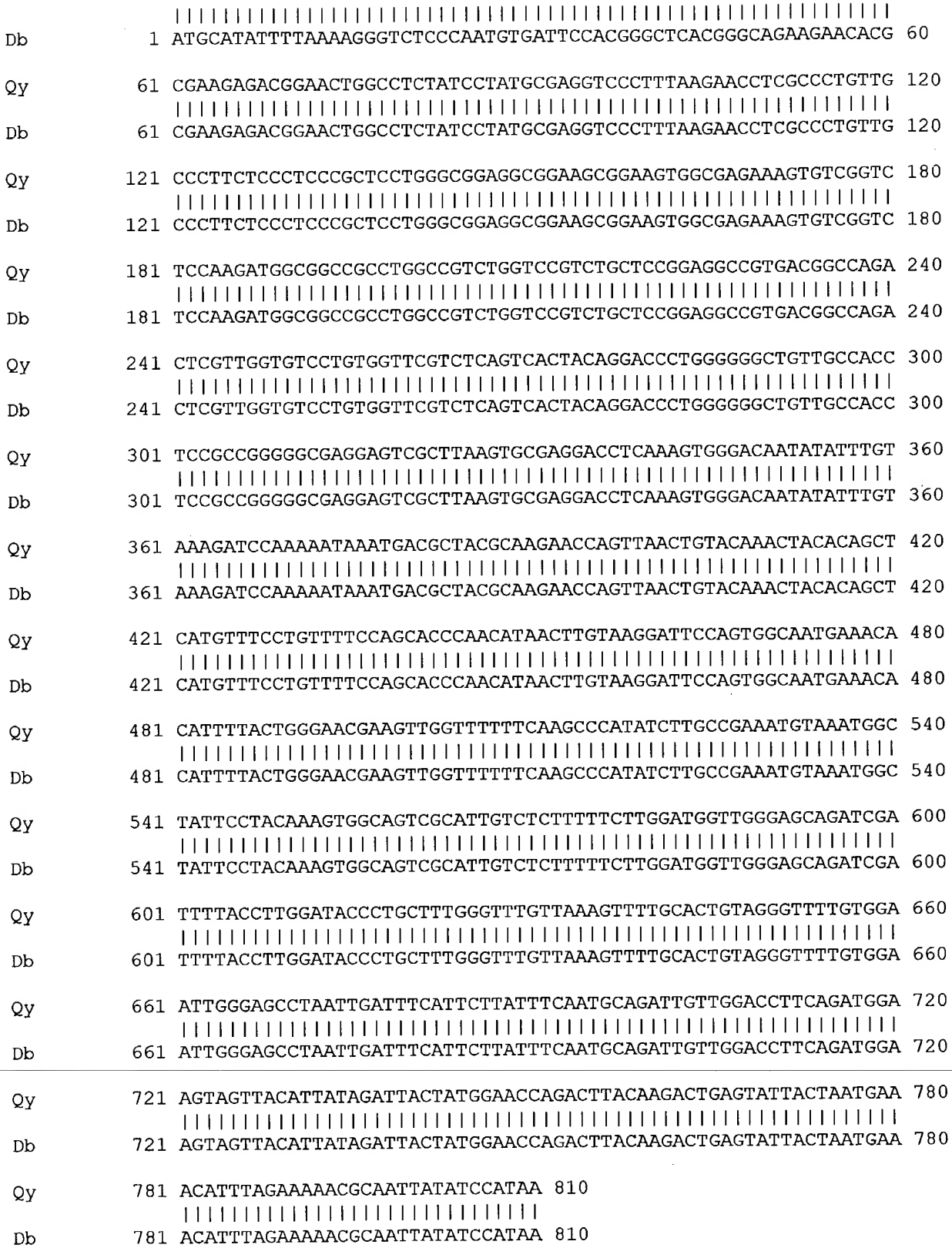

Db 1 ATGCATATTTTAAAAGGGTCTCCCAATGTGATTCCACGGGCTCACGGGCAGAAGAACACG 60
Qy 61 CGAAGAGACGGAACTGGCCTCTATCCTATGCGAGGTCCCTTTAAGAACCTCGCCCTGTTG 120
Db 61 CGAAGAGACGGAACTGGCCTCTATCCTATGCGAGGTCCCTTTAAGAACCTCGCCCTGTTG 120
Qy 121 CCCTTCTCCCTCCCGCTCCTGGGCGGAGGCGGAAGCGGAAGTGGCGAGAAAGTGTCGGTC 180
Db 121 CCCTTCTCCCTCCCGCTCCTGGGCGGAGGCGGAAGCGGAAGTGGCGAGAAAGTGTCGGTC 180
Qy 181 TCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGCCAGA 240
Db 181 TCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGCCAGA 240
Qy 241 CTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCTGTTGCCACC 300
Db 241 CTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCTGTTGCCACC 300
Qy 301 TCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGT 360
Db 301 TCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGT 360
Qy 361 AAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCT 420
Db 361 AAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCT 420
Qy 421 CATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACA 480
Db 421 CATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACA 480
Qy 481 CATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGC 540
Db 481 CATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGC 540
Qy 541 TATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGA 600
Db 541 TATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGA 600
Qy 601 TTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGA 660
Db 601 TTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGA 660
Qy 661 ATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGA 720
Db 661 ATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGA 720
Qy 721 AGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAA 780
Db 721 AGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAA 780
Qy 781 ACATTTAGAAAAACGCAATTATATCCATAA 810
Db 781 ACATTTAGAAAAACGCAATTATATCCATAA 810

RESULT 3

AAD51940
ID AAD51940 standard; cDNA; 810 BP.
XX
AC AAD51940;
XX
DT 02-MAY-2003 (first entry)
XX
DE Human BBP-1 cDNA.
XX
KW Human; beta-amyloid peptide-binding protein; BAP; Abeta; betaAP; BBP;
KW Alzheimer's disease; AD; transgenic; transgenic animal; gene therapy;
KW neuroprotective; nootropic; gene; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1. .810
FT   /*tag= a
FT   /product= "Human BBP-1"
XX
PN WO200290499-A2.
XX
PD 14-NOV-2002.
XX
PF 06-MAY-2002; 2002WO-US014223.
XX
PR 09-MAY-2001; 2001US-00852100.
XX
PA (AMHP) WYETH.
XX
PI Ozenberger BA, Bard JA, Kajkowski EM, Jacobsen JS, Walker SG;
PI Sofia HJ, Howland DS;
XX
DR WPI; 2003-120537/11.
DR P-PSDB; AAE33877.
XX
PT New human beta-amyloid peptide-binding protein, useful for diagnosing
PT and/or treating diseases associated with aberrant expression of beta-
PT amyloid peptide, e.g. Alzheimer's disease.
XX
PS Claim 1; Page 82-84; 85pp; English.
XX
CC The present invention relates to novel human beta-amyloid peptide (BAP;
CC Abeta, betaAP)-binding (BBP) proteins and polynucleotides encoding such
CC proteins. BBP sequences are useful to diagnose and/or treat diseases
CC associated with aberrant expression of human BAP such as Alzheimer's
CC disease (AD). They are used to generate transgenic animals. Sequences of
CC the invention are also used in gene therapy. The present sequence is
CC human BBP-1 cDNA
XX
SQ Sequence 810 BP; 204 A; 183 C; 202 G; 221 T; 0 U; 0 Other;

  Query Match   100.0%; Score 810; DB 7; Length 810;
  Best Local Similarity   100.0%; Pred. No. 2e-233;
  Matches 810; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ATGCATATTTTAAAAGGGTCTCCCAATGTGATTCCACGGGCTCACGGGCAGAAGAACACG 60


Db 1 ATGCATATTTTAAAAGGGTCTCCCAATGTGATTCCACGGGCTCACGGGCAGAAGAACACG 60
Qy 61 CGAAGAGACGGAACTGGCCTCTATCCTATGCGAGGTCCCTTTAAGAACCTCGCCCTGTTG 120
Db 61 CGAAGAGACGGAACTGGCCTCTATCCTATGCGAGGTCCCTTTAAGAACCTCGCCCTGTTG 120
Qy 121 CCCTTCTCCCTCCCGCTCCTGGGCGGAGGCGGAAGCGGAAGTGGCGAGAAAGTGTCGGTC 180
Db 121 CCCTTCTCCCTCCCGCTCCTGGGCGGAGGCGGAAGCGGAAGTGGCGAGAAAGTGTCGGTC 180
Qy 181 TCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGCCAGA 240
Db 181 TCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGCCAGA 240
Qy 241 CTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCTGTTGCCACC 300
Db 241 CTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCTGTTGCCACC 300
Qy 301 TCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGT 360
Db 301 TCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGT 360
Qy 361 AAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCT 420
Db 361 AAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCT 420
Qy 421 CATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACA 480
Db 421 CATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACA 480
Qy 481 CATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGC 540
Db 481 CATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGC 540
Qy 541 TATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGA 600
Db 541 TATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGA 600
Qy 601 TTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGA 660
Db 601 TTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGA 660
Qy 661 ATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGA 720
Db 661 ATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGA 720
Qy 721 AGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAA 780
Db 721 AGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAA 780
Qy 781 ACATTTAGAAAAACGCAATTATATCCATAA 810
Db 781 ACATTTAGAAAAACGCAATTATATCCATAA 810

RESULT 4

AAD51979
ID AAD51979 standard; DNA; 1246 BP.
XX
AC AAD51979;
XX
DT 02-MAY-2003 (first entry)
XX
DE Human BBP-1 genomic DNA.
XX
KW Human; beta-amyloid peptide-binding protein; BAP; Abeta; betaAP; BBP;
KW Alzheimer's disease; AD; transgenic; transgenic animal; gene therapy;
KW neuroprotective; nootropic; ds.
XX
OS Homo sapiens.
XX
PN WO200290499-A2.
XX
PD 14-NOV-2002.
XX
PF 06-MAY-2002; 2002WO-US014223.
XX
PR 09-MAY-2001; 2001US-00852100.
XX
PA (AMHP) WYETH.
XX
PI Ozenberger BA, Bard JA, Kajkowski EM, Jacobsen JS, Walker SG;
PI Sofia HJ, Howland DS;
XX
DR WPI; 2003-120537/11.
XX
PT New human beta-amyloid peptide-binding protein, useful for diagnosing
PT and/or treating diseases associated with aberrant expression of beta-
PT amyloid peptide, e.g. Alzheimer's disease.
XX
PS Disclosure; Fig 11; 85pp; English.
XX
CC The present invention relates to novel human beta-amyloid peptide (BAP;
CC Abeta, betaAP)-binding (BBP) proteins and polynucleotides encoding such
CC proteins. BBP sequences are useful to diagnose and/or treat diseases
CC associated with aberrant expression of human BAP such as Alzheimer's
CC disease (AD). They are used to generate transgenic animals. Sequences of
CC the invention are also used in gene therapy. The present sequence is
CC human BBP-1 genomic DNA
XX
SQ Sequence 1246 BP; 318 A; 255 C; 283 G; 390 T; 0 U; 0 Other;

Query Match 100.0%; Score 810; DB 7; Length 1246;
Best Local Similarity 100.0%; Pred. No. 2.6e-233;
Matches 810; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGCATATTTTAAAAGGGTCTCCCAATGTGATTCCACGGGCTCACGGGCAGAAGAACACG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 ATGCATATTTTAAAAGGGTCTCCCAATGTGATTCCACGGGCTCACGGGCAGAAGAACACG 177

Qy         61 CGAAGAGACGGAACTGGCCTCTATCCTATGCGAGGTCCCTTTAAGAACCTCGCCCTGTTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 CGAAGAGACGGAACTGGCCTCTATCCTATGCGAGGTCCCTTTAAGAACCTCGCCCTGTTG 237
```

```
Qy        121 CCCTTCTCCCTCCCGCTCCTGGGCGGAGGCGGAAGCGGAAGTGGCGAGAAAGTGTCGGTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 CCCTTCTCCCTCCCGCTCCTGGGCGGAGGCGGAAGCGGAAGTGGCGAGAAAGTGTCGGTC 297

Qy        181 TCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGCCAGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 TCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGCCAGA 357

Qy        241 CTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCTGTTGCCACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 CTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCTGTTGCCACC 417

Qy        301 TCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 TCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGT 477

Qy        361 AAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 AAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCT 537

Qy        421 CATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 CATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACA 597

Qy        481 CATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        598 CATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGC 657

Qy        541 TATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 TATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGA 717

Qy        601 TTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        718 TTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGA 777

Qy        661 ATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        778 ATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGA 837

Qy        721 AGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        838 AGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAA 897

Qy        781 ACATTTAGAAAAACGCAATTATATCCATAA 810
              ||||||||||||||||||||||||||||||
Db        898 ACATTTAGAAAAACGCAATTATATCCATAA 927
```

RESULT 5
AAX97705
ID AAX97705 standard; DNA; 970 BP.
XX
AC AAX97705;
XX
DT 13-SEP-1999 (first entry)

XX
DE Extended human secreted protein coding sequence, SEQ ID NO. 270.
XX
KW Secreted protein; human; cytokine; cellular proliferation; cell movement;
KW cellular differentiation; immune system regulator; anti-inflammatory;
KW haematopoiesis regulator; tissue growth regulator; tumour inhibitor;
KW reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy;
KW genetic disease; ss.
XX
OS Homo sapiens.
XX
PN WO9931236-A2.
XX
PD 24-JUN-1999.
XX
PF 17-DEC-1998; 98WO-IB002122.
XX
PR 17-DEC-1997; 97US-0069957P.
PR 09-FEB-1998; 98US-0074121P.
PR 13-APR-1998; 98US-0081563P.
PR 10-AUG-1998; 98US-0096116P.
XX
PA (GEST) GENSET.
XX
PI Bougueleret L, Duclert A, Dumas Milne Edwards J;
XX
DR WPI; 1999-385906/32.
DR P-PSDB; AAY36021.
XX
PT New isolated human secreted proteins.
XX
PS Claim 1; Page 346-347; 516pp; English.
XX
CC This sequence represents an extended human secreted protein coding
CC sequence of the invention. The secreted proteins can be used in treating
CC or controlling a variety of human conditions. The secreted proteins may
CC act as cytokines or may affect cellular proliferation or differentiation
CC or may act as immune system regulators, haematopoiesis regulators, tissue
CC growth regulators, regulators of reproductive hormones or cell movement
CC or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or
CC tumour inhibition activity. The DNAs can be used in forensic procedures
CC to identify individuals or in diagnostic procedures to identify
CC individuals having genetic diseases resulting from abnormal expression of
CC the genes corresponding to the extended cDNAs. They are also useful for
CC constructing a high resolution map of the human chromosomes. They can
CC also be used for gene therapy to control or treat genetic diseases
XX
SQ Sequence 970 BP; 267 A; 173 C; 199 G; 323 T; 0 U; 8 Other;

Query Match 74.4%; Score 602.8; DB 2; Length 970;
Best Local Similarity 98.4%; Pred. No. 6.7e-171;
Matches 624; Conservative 5; Mismatches 3; Indels 2; Gaps 2;

```
Qy        177 GGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGC 236
              ||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db          2 GGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGKCTGCTCCGGAGGCCGTGACGGC 61
```

```
Qy        237 CAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCTGTTGC 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCTGTTGC 121

Qy        297 CACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATAT 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 CACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATAT 181

Qy        357 TTGTAAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACAC 416
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 TTGTAAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACAC 241

Qy        417 AGCTCATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGA 476
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 AGCTCATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGA 301

Qy        477 AACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAA 536
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 AACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAA 361

Qy        537 TGGCTATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGA 596
              |||||||||||||| |  |||||||| ||||||||||||||||||||||||||||||||
Db        362 TGGCTATTCCTACAATG-AGCAGTCGCA-TGTCTCTTTTTCTTGGATGGTTGGGAGCAGA 419

Qy        597 TCGATTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTG 656
              ||||||||||||||||||||||||||||||||||||:|||:|||||||||||||||:|
Db        420 TCGATTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAABTTTYGCACTGTAGGGTTTKG 479

Qy        657 TGGAATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGA 716
              ||||||||||||||||||||||||:|||||||||||||||||||||||||||||||| |
Db        480 TGGAATTGGGAGCCTAATTGATTTCATYCTTATTTCAATGCAGATTGTTGGACCTTCAAA 539

Qy        717 TGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAA 776
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 TGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAA 599

Qy        777 TGAAACATTTAGAAAAACGCAATTATATCCATAA 810
              |||||||||||||||||||||||||||||||||
Db        600 TGAAACATTTAGAAAAACGCAATTATATCCATAA 633
```

RESULT 6
AAA77946
ID AAA77946 standard; cDNA; 508 BP.
XX
AC AAA77946;
XX
DT 14-NOV-2000 (first entry)
XX
DE cDNA encoding human colon tumour polypeptide, SEQ ID NO:233.
XX
KW Human colon tumour polypeptide; tumour antigen; cancer; vaccine;
KW immunotherapy; diagnosis; progression; ss.
XX
OS Homo sapiens.
XX
PN WO200037643-A2.

XX
PD 29-JUN-2000.
XX
PF 23-DEC-1999; 99WO-US030909.
XX
PR 23-DEC-1998; 98US-00221298.
PR 02-JUL-1999; 99US-00347496.
PR 22-SEP-1999; 99US-00401064.
PR 19-NOV-1999; 99US-00444242.
PR 02-DEC-1999; 99US-00454150.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk J;
PI Wang T, Yuqiu J;
XX
DR WPI; 2000-442671/38.
XX
PT New colon tumor polypeptides used to inhibit the development of cancer,
PT especially colon cancer, and for diagnosing and monitoring the
PT progression of the cancer.
XX
PS Claim 1; Page 158-159; 229pp; English.
XX
CC Sequences AAA77722-A78199 represent 478 cDNAs encoding proteins or
CC portions of proteins which are associated with human colon tumours. The
CC invention also specifically discloses 8 human colon tumour proteins
CC (AAB11897-B11904). The nucleic acids, the polypeptides they encode, and
CC antigen presenting cells (APCs, preferably dendritic cells) expressing
CC such polypeptides may be used in vaccines that target tumour cells,
CC especially colon tumour cells, thereby inhibiting the development of
CC cancer. T-cells specific for the polypeptide expressed by the APC are
CC used to remove tumour cells from biological samples, especially blood or
CC fractions thereof. The sample or the isolated T-cells specific for the
CC polypeptide can then be used to inhibit cancer development. CD4+ and/or
CC CD8+ T-cells from a patient may be incubated with a polypeptide or
CC nucleic acid of the invention, or an APC expressing such a polypeptide,
CC to cause the proliferation of specific T-cells. The T-cells can be cloned
CC and then administered back to the patient to inhibit cancer development.
CC Nucleic acids encoding the polypeptides and antibodies against the
CC polypeptides may be used to determine the expression level of a tumour
CC protein of the invention, and therefore to determine whether cancer cells
CC are present. Such diagnostic methods may also be used to monitor the
CC progression of a cancer by repeating the processes at time intervals, and
CC comparing the current result to previous results. The present sequence
CC represents a cDNA encoding a human colon tumour polypeptide
XX
SQ Sequence 508 BP; 153 A; 89 C; 103 G; 163 T; 0 U; 0 Other;

Query Match 61.6%; Score 499; DB 3; Length 508;
Best Local Similarity 100.0%; Pred. No. 9.4e-140;
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 312 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 371
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 60

```
Qy        372 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 120

Qy        432 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 180

Qy        492 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 240

Qy        552 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 611
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 300

Qy        612 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 360

Qy        672 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 731
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 420

Qy        732 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 791
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 480

Qy        792 AACGCAATTATATCCATAA 810
              ||||||||||||||||||
Db        481 AACGCAATTATATCCATAA 499
```

RESULT 7
AAA77958
ID AAA77958 standard; cDNA; 508 BP.
XX
AC AAA77958;
XX
DT 14-NOV-2000 (first entry)
XX
DE cDNA encoding human colon tumour polypeptide, SEQ ID NO:245.
XX
KW Human colon tumour polypeptide; tumour antigen; cancer; vaccine;
KW immunotherapy; diagnosis; progression; ss.
XX
OS Homo sapiens.
XX
PN WO200037643-A2.
XX
PD 29-JUN-2000.
XX
PF 23-DEC-1999; 99WO-US030909.
XX
PR 23-DEC-1998; 98US-00221298.
PR 02-JUL-1999; 99US-00347496.
PR 22-SEP-1999; 99US-00401064.

PR 19-NOV-1999; 99US-00444242.
PR 02-DEC-1999; 99US-00454150.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk J;
PI Wang T, Yuqiu J;
XX
DR WPI; 2000-442671/38.
XX
PT New colon tumor polypeptides used to inhibit the development of cancer,
PT especially colon cancer, and for diagnosing and monitoring the
PT progression of the cancer.
XX
PS Claim 1; Page 162; 229pp; English.
XX
CC Sequences AAA77722-A78199 represent 478 cDNAs encoding proteins or
CC portions of proteins which are associated with human colon tumours. The
CC invention also specifically discloses 8 human colon tumour proteins
CC (AAB11897-B11904). The nucleic acids, the polypeptides they encode, and
CC antigen presenting cells (APCs, preferably dendritic cells) expressing
CC such polypeptides may be used in vaccines that target tumour cells,
CC especially colon tumour cells, thereby inhibiting the development of
CC cancer. T-cells specific for the polypeptide expressed by the APC are
CC used to remove tumour cells from biological samples, especially blood or
CC fractions thereof. The sample or the isolated T-cells specific for the
CC polypeptide can then be used to inhibit cancer development. CD4+ and/or
CC CD8+ T-cells from a patient may be incubated with a polypeptide or
CC nucleic acid of the invention, or an APC expressing such a polypeptide,
CC to cause the proliferation of specific T-cells. The T-cells can be cloned
CC and then administered back to the patient to inhibit cancer development.
CC Nucleic acids encoding the polypeptides and antibodies against the
CC polypeptides may be used to determine the expression level of a tumour
CC protein of the invention, and therefore to determine whether cancer cells
CC are present. Such diagnostic methods may also be used to monitor the
CC progression of a cancer by repeating the processes at time intervals, and
CC comparing the current result to previous results. The present sequence
CC represents a cDNA encoding a human colon tumour polypeptide
XX
SQ Sequence 508 BP; 153 A; 89 C; 103 G; 163 T; 0 U; 0 Other;

Query Match 61.6%; Score 499; DB 3; Length 508;
Best Local Similarity 100.0%; Pred. No. 9.4e-140;
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        312 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 60

Qy        372 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 120

Qy        432 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 180
```

```
Qy        492 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 240

Qy        552 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 611
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 300

Qy        612 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 360

Qy        672 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 731
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 420

Qy        732 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 791
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 480

Qy        792 AACGCAATTATATCCATAA 810
              ||||||||||||||||||
Db        481 AACGCAATTATATCCATAA 499
```

RESULT 8
AAI28684
ID AAI28684 standard; cDNA; 508 BP.
XX
AC AAI28684;
XX
DT 12-OCT-2001 (first entry)
XX
DE Colon tumour related determined cDNA sequence for clone 25275.
XX
KW Human; immunotherapy; diagnosis; colon cancer; colon tumour; immunogenic;
KW gene therapy; vaccine; colonic cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200149716-A2.
XX
PD 12-JUL-2001.
XX
PF 29-DEC-2000; 2000WO-US035596.
XX
PR 30-DEC-1999; 99US-00476296.
PR 10-JAN-2000; 2000US-00480321.
PR 15-FEB-2000; 2000US-00504629.
PR 06-MAR-2000; 2000US-00519444.
PR 19-MAY-2000; 2000US-00575251.
PR 29-JUN-2000; 2000US-00609448.
PR 28-AUG-2000; 2000US-00649811.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk JA;

PI King GE, Wang T, Jiang Y;
XX
DR WPI; 2001-441847/47.
XX
PT Colon tumor associated proteins and nucleic acids useful for the
PT prevention, diagnosis and treatment of colonic cancer.
XX
PS Claim 2; Page 198; 472pp; English.
XX
CC The present invention describes colon tumour associated proteins (I) and
CC the polynucleotides (II) that encode them. (I) have cytostatic activity.
CC (I) and (II) can be used in gene therapy and vaccine production. (I) and
CC (II) may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate colon tumour associated protein (TCAP)
CC expression, such as colonic cancer. For example, (I) and (II) may be used
CC to treat disorders associated with decreased expression by rectifying
CC mutations or deletions in a patient's genome that affect the activity of
CC TCAPs by expressing inactive proteins or to supplement the patients own
CC production of them. Additionally, (II) may be used to produce the TCAP
CC proteins, by inserting the nucleic acids into a host cell culturing the
CC cell to express the protein. (II) and its complementary sequences may
CC also be used as DNA probes in diagnostic polymerase chain reaction (PCR)
CC and hybridisation assays to detect and quantitate the presence of similar
CC nucleic acids in samples, and therefore which patients may be in need of
CC restorative therapy. (I) may also be used as antigens in the production
CC of antibodies against TCAPs and in assays to identify modulators of TCAP
CC expression and activity. Anti-(I) antibodies and antagonists may also be
CC used to down regulate TCAP expression and activity. The anti-(I)
CC antibodies may also be used as diagnostic agents for detecting the
CC presence of TCAPs in samples (e.g. by enzyme linked immunosorbant assay
CC (ELISA)). AAI28460 to AAI29512 and AAM24494 to AAM24523 represent
CC nucleotide and amino acid sequences given in the exemplification of the
CC present invention
XX
SQ Sequence 508 BP; 153 A; 89 C; 103 G; 163 T; 0 U; 0 Other;

Query Match 61.6%; Score 499; DB 4; Length 508;
Best Local Similarity 100.0%; Pred. No. 9.4e-140;
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        312 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 60

Qy        372 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 120

Qy        432 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 180

Qy        492 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 240

Qy        552 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 611
```

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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 300

Qy        612 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 671
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 360

Qy        672 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 731
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 420

Qy        732 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 791
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 480

Qy        792 AACGCAATTATATCCATAA 810
                    ||||||||||||||||||
Db        481 AACGCAATTATATCCATAA 499
```

RESULT 9
AAI28696
ID AAI28696 standard; cDNA; 508 BP.
XX
AC AAI28696;
XX
DT 12-OCT-2001 (first entry)
XX
DE Colon tumour related determined cDNA sequence for clone 25288.
XX
KW Human; immunotherapy; diagnosis; colon cancer; colon tumour; immunogenic;
KW gene therapy; vaccine; colonic cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200149716-A2.
XX
PD 12-JUL-2001.
XX
PF 29-DEC-2000; 2000WO-US035596.
XX
PR 30-DEC-1999; 99US-00476296.
PR 10-JAN-2000; 2000US-00480321.
PR 15-FEB-2000; 2000US-00504629.
PR 06-MAR-2000; 2000US-00519444.
PR 19-MAY-2000; 2000US-00575251.
PR 29-JUN-2000; 2000US-00609448.
PR 28-AUG-2000; 2000US-00649811.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk JA;
PI King GE, Wang T, Jiang Y;
XX
DR WPI; 2001-441847/47.
XX
PT Colon tumor associated proteins and nucleic acids useful for the

PT prevention, diagnosis and treatment of colonic cancer.
XX
PS Claim 2; Page 201; 472pp; English.
XX
CC The present invention describes colon tumour associated proteins (I) and
CC the polynucleotides (II) that encode them. (I) have cytostatic activity.
CC (I) and (II) can be used in gene therapy and vaccine production. (I) and
CC (II) may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate colon tumour associated protein (TCAP)
CC expression, such as colonic cancer. For example, (I) and (II) may be used
CC to treat disorders associated with decreased expression by rectifying
CC mutations or deletions in a patient's genome that affect the activity of
CC TCAPs by expressing inactive proteins or to supplement the patients own
CC production of them. Additionally, (II) may be used to produce the TCAP
CC proteins, by inserting the nucleic acids into a host cell culturing the
CC cell to express the protein. (II) and its complementary sequences may
CC also be used as DNA probes in diagnostic polymerase chain reaction (PCR)
CC and hybridisation assays to detect and quantitate the presence of similar
CC nucleic acids in samples, and therefore which patients may be in need of
CC restorative therapy. (I) may also be used as antigens in the production
CC of antibodies against TCAPs and in assays to identify modulators of TCAP
CC expression and activity. Anti-(I) antibodies and antagonists may also be
CC used to down regulate TCAP expression and activity. The anti-(I)
CC antibodies may also be used as diagnostic agents for detecting the
CC presence of TCAPs in samples (e.g. by enzyme linked immunosorbant assay
CC (ELISA)). AAI28460 to AAI29512 and AAM24494 to AAM24523 represent
CC nucleotide and amino acid sequences given in the exemplification of the
CC present invention
XX
SQ Sequence 508 BP; 153 A; 89 C; 103 G; 163 T; 0 U; 0 Other;

Query Match 61.6%; Score 499; DB 4; Length 508;
Best Local Similarity 100.0%; Pred. No. 9.4e-140;
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        312 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 60

Qy        372 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 120

Qy        432 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 180

Qy        492 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 240

Qy        552 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 611
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 300

Qy        612 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        301 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 360

Qy        672 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 731
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 420

Qy        732 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 791
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 480

Qy        792 AACGCAATTATATCCATAA 810
              ||||||||||||||||||
Db        481 AACGCAATTATATCCATAA 499
```

RESULT 10
ABZ32882
ID ABZ32882 standard; cDNA; 508 BP.
XX
AC ABZ32882;
XX
DT 30-JAN-2003 (first entry)
XX
DE Human colon tumour cDNA clone 25288 SEQ ID NO:245.
XX
KW Human; colon cancer; colon tumour; immunotherapy; diagnosis; cancer;
KW tumour; immune response; immunostimulant; cytostatic; vaccine; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200283070-A2.
XX
PD 24-OCT-2002.
XX
PF 09-APR-2002; 2002WO-US011475.
XX
PR 10-APR-2001; 2001US-00833263.
PR 03-AUG-2001; 2001US-00922217.
PR 19-DEC-2001; 2001US-00025380.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk JA;
PI Wang T, Jiang Y, Smith CL, King GE, Wang A, Clapper JD, Skeiky YAW;
PI Fanger GR, Vedvick TS, Carter D;
XX
DR WPI; 2003-067548/06.
XX
PT New polynucleotide, useful for the preparation of a composition for
PT stimulating an immune response against, or treating, cancer.
XX
PS Example 1; Page 204; 537pp; English.
XX
CC The present invention describes compounds (I) for the immunotherapy and
CC diagnosis of colon cancer. Also described: (1) a method for detecting the
CC presence of cancer in a patient; (2) a method for stimulating and/or
CC expanding T cells specific for a tumour protein; (3) an isolated T cell

CC population comprising T cells prepared by the method of (2); (4) a method
CC for stimulating an immune response in a patient; (5) a method for
CC treating cancer in a patient; and (6) a method for inhibiting the
CC development of cancer in a patient. (I) have immunostimulant and
CC cytostatic activities and can be used in vaccines. ABZ32646 to ABZ33725
CC and ABP55343 to ABP55391 represent human colon cancer/tumour related
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 508 BP; 153 A; 89 C; 103 G; 163 T; 0 U; 0 Other;

Query Match 61.6%; Score 499; DB 7; Length 508;
Best Local Similarity 100.0%; Pred. No. 9.4e-140;
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        312 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 60

Qy        372 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 120

Qy        432 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 180

Qy        492 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 240

Qy        552 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 611
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 300

Qy        612 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 360

Qy        672 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 731
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 420

Qy        732 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 791
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 480

Qy        792 AACGCAATTATATCCATAA 810
              ||||||||||||||||||
Db        481 AACGCAATTATATCCATAA 499
```

RESULT 11
ABZ32870
ID ABZ32870 standard; cDNA; 508 BP.
XX
AC ABZ32870;
XX

DT 30-JAN-2003 (first entry)
XX
DE Human colon tumour cDNA clone 25275 SEQ ID NO:233.
XX
KW Human; colon cancer; colon tumour; immunotherapy; diagnosis; cancer;
KW tumour; immune response; immunostimulant; cytostatic; vaccine; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200283070-A2.
XX
PD 24-OCT-2002.
XX
PF 09-APR-2002; 2002WO-US011475.
XX
PR 10-APR-2001; 2001US-00833263.
PR 03-AUG-2001; 2001US-00922217.
PR 19-DEC-2001; 2001US-00025380.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk JA;
PI Wang T, Jiang Y, Smith CL, King GE, Wang A, Clapper JD, Skeiky YAW;
PI Fanger GR, Vedvick TS, Carter D;
XX
DR WPI; 2003-067548/06.
XX
PT New polynucleotide, useful for the preparation of a composition for
PT stimulating an immune response against, or treating, cancer.
XX
PS Example 1; Page 201; 537pp; English.
XX
CC The present invention describes compounds (I) for the immunotherapy and
CC diagnosis of colon cancer. Also described: (1) a method for detecting the
CC presence of cancer in a patient; (2) a method for stimulating and/or
CC expanding T cells specific for a tumour protein; (3) an isolated T cell
CC population comprising T cells prepared by the method of (2); (4) a method
CC for stimulating an immune response in a patient; (5) a method for
CC treating cancer in a patient; and (6) a method for inhibiting the
CC development of cancer in a patient. (I) have immunostimulant and
CC cytostatic activities and can be used in vaccines. ABZ32646 to ABZ33725
CC and ABP55343 to ABP55391 represent human colon cancer/tumour related
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 508 BP; 153 A; 89 C; 103 G; 163 T; 0 U; 0 Other;

Query Match 61.6%; Score 499; DB 7; Length 508;
Best Local Similarity 100.0%; Pred. No. 9.4e-140;
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        312 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 60

Qy        372 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 120
```

```
Qy        432 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 180

Qy        492 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 240

Qy        552 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 611
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 300

Qy        612 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 360

Qy        672 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 731
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 420

Qy        732 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 791
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 480

Qy        792 AACGCAATTATATCCATAA 810
              ||||||||||||||||||
Db        481 AACGCAATTATATCCATAA 499
```

```
RESULT 12
ABK52558
ID   ABK52558 standard; cDNA; 1095 BP.
XX
AC   ABK52558;
XX
DT   13-AUG-2002  (first entry)
XX
DE   cDNA encoding RNA polymerase II subunit 11.
XX
KW   RNA polymerase II subunit 11; ss; gene; cancer; HIV; infection;
KW   human immunodeficiency virus.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   CDS             12. .314
FT                   /*tag=  a
FT                   /product= "RNA polymerase II subunit 11"
XX
PN   CN1331300-A.
XX
PD   16-JAN-2002.
XX
PF   30-JUN-2000; 2000CN-00116963.
XX
PR   30-JUN-2000; 2000CN-00116963.
```

XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-340664/38.
DR P-PSDB; AAU97631.
XX
PT Polypeptide-RNA polymerase II subunit 11 and polynucleotide for coding
PT it.
XX
PS Claim 6; Page 28-29; 32pp; Chinese.
XX
CC This invention relates to the DNA and protein sequences of a novel
CC polypeptide-RNA polymerase II subunit 11 protein. The invention also
CC comprises a process for preparing the polypeptide of the invention by DNA
CC recombination, the application of the polypeptide in treating diseases
CC such as cancer, human immunodeficiency virus (HIV) infection, etc, the
CC antagonist of the polypeptide and its medical action, and the application
CC of the said polynucleotide are disclosed. The present sequence represents
CC the cDNA sequence encoding the RNA polymerase II subunit 11 protein of
CC the invention
XX
SQ Sequence 1095 BP; 268 A; 230 C; 244 G; 353 T; 0 U; 0 Other;

Query Match 54.6%; Score 442.2; DB 6; Length 1095;
Best Local Similarity 81.1%; Pred. No. 1.9e-122;
Matches 596; Conservative 0; Mismatches 38; Indels 101; Gaps 3;

```
Qy        177 GGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGC 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db          2 GGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGATGCCGTGACGGC 61

Qy        237 CAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCTGTTGC 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCTGTTGC 121

Qy        297 CACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATAT-A 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        122 CACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATCC 181

Qy        356 TTTGTAAAGATCCAAAAATAAATGACGCTA----------CGCAAGAACCAGTTAA 401
              | |||  ||| |        |  || || |             |||     | |   |
Db        182 TCTGTGGAGAACACCCCCCCATGGAGGCGAGGGTCTTACTCTGTCGCCCTGGCTGGAGTA 241

Qy        402 CTGTACAAACTACACAGCTCA---------------------------------------- 422
              | ||   |    | |||||||
Db        242 CAGTGGCACGATCTCAGCTCACTGCAGCCTCCGCCTCCCGGGTTCAGTCAATTCTCCTGC 301

Qy        423 ----------------------------------------------TGTTTCCTGTTTT 435
                                                           ||||||||||||
Db        302 CTCAGCCTCCTGAGTAGCTGGGACTACAGGCATGCGCCACCACACCCGGTTTCCTGTTTT 361

Qy        436 CCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGGGAAC 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 CCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGGGAAC 421
```

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Qy        496 GAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAAAGTG 555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 GAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAAAGTG 481

Qy        556 GCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGGATAC 615
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 GCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGGATAC 541

Qy        616 CCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCTAATT 675
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 CCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCTAATT 601

Qy        676 GATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACATTATA 735
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 GATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACATTATA 661

Qy        736 GATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAAAACG 795
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        662 GATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAAAACG 721

Qy        796 CAATTATATCCATAA 810
              ||||||||||||||
Db        722 CAATTATATCCATAA 736
```

RESULT 13
AAX41191
ID AAX41191 standard; cDNA; 440 BP.
XX
AC AAX41191;
XX
DT 17-JUN-1999 (first entry)
XX
DE Human secreted protein 5' EST SEQ ID NO:135.
XX
KW Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW forensic; gene therapy; chromosome mapping; signal peptide;
KW upstream regulatory sequence; cytokine activity; cell proliferation;
KW differentiation; haematopoiesis regulation; tissue growth regulation;
KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; anti-inflammatory; tumour inhibition; ds.
XX
OS Homo sapiens.
XX
PN WO9906548-A2.
XX
PD 11-FEB-1999.
XX
PF 31-JUL-1998; 98WO-IB001222.
XX
PR 01-AUG-1997; 97US-00905135.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Lacroix B;
XX
DR WPI; 1999-153778/13.

DR P-PSDB; AAY12358.
XX
PT New nucleic acids encoding human secreted proteins - obtained from cDNA
PT libraries prepared from e.g. liver, ovary, brain, prostate, kidney, lung,
PT umbilical cord, placenta and colon tissue.
XX
PS Claim 1; Page 315; 824pp; English.
XX
CC AAX41094 to AAX41347 represent 5' expressed sequence tags (ESTs) for
CC human secreted proteins, and encode the proteins given in AAY12261 to
CC AAY12514, respectively. The proteins given represent the signal peptide
CC and an N-terminal fragment of a secreted protein. The nucleic acid
CC sequences can be used for producing secreted human gene products. They
CC can also be used to develop products for diagnosis and therapy. The
CC proteins obtained may have cytokine activity, cell
CC proliferation/differentiation activity, haematopoiesis regulating
CC activity, tissue growth regulating activity, reproductive hormone
CC regulating activity, chemotactic/ chemokinetic activity, haemostatic and
CC thrombolytic activity, receptor/ ligand activity, anti-inflammatory
CC activity, tumour inhibition activity or other activities. The products
CC can be used in forensic, gene therapy and chromosome mapping procedures.
CC The sequences can also be used for obtaining corresponding promoter
CC sequences. The nucleic acids encoding the signal peptide can be used for
CC directing extracellular secretion of a polypeptide or the insertion of a
CC polypeptide into a membrane, or importing a polypeptide into a cell
XX
SQ Sequence 440 BP; 107 A; 103 C; 114 G; 114 T; 0 U; 2 Other;

Query Match 53.9%; Score 436.8; DB 2; Length 440;
Best Local Similarity 99.5%; Pred. No. 4.9e-121;
Matches 436; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy        166 GAGAAAGTGTCGGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGAG 225
              ||||||||||||||||||||||||||||||||||||::|||||||||||||||||||||
Db          3 GAGAAAGTGTCGGTCTCCAAGATGGCGGCCGCCTGGCSDTCTGGTCCGTCTGCTCCGGAG 62

Qy        226 GCCGTGACGGCCAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGG 285
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 GCCGTGACGGCCAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGG 122

Qy        286 GGGGCTGTTGCCACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTG 345
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 GGGGCTGTTGCCACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTG 182

Qy        346 GGACAATATATTTGTAAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAACTGT 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 GGACAATATATTTGTAAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAACTGT 242

Qy        406 ACAAACTACACAGCTCATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGGATTCC 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 ACAAACTACACAGCTCATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGGATTCC 302

Qy        466 AGTGGCAATGAAACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTGC 525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 AGTGGCAATGAAACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTGC 362

Qy        526 CGAAATGTAAATGGCTATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGG 585
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 CGAAATGTAAATGGCTATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGG 422

Qy        586 TTGGGAGCAGATCGATTT 603
                    ||||||||||||||||||
Db        423 TTGGGAGCAGATCGATTT 440


RESULT 14
AAX41259
ID   AAX41259 standard; cDNA; 455 BP.
XX
AC   AAX41259;
XX
DT   17-JUN-1999  (first entry)
XX
DE   Human secreted protein 5' EST SEQ ID NO:203.
XX
KW   Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW   forensic; gene therapy; chromosome mapping; signal peptide;
KW   upstream regulatory sequence; cytokine activity; cell proliferation;
KW   differentiation; haematopoiesis regulation; tissue growth regulation;
KW   reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW   thrombolytic; anti-inflammatory; tumour inhibition; ds.
XX
OS   Homo sapiens.
XX
PN   WO9906548-A2.
XX
PD   11-FEB-1999.
XX
PF   31-JUL-1998;   98WO-IB001222.
XX
PR   01-AUG-1997;   97US-00905135.
XX
PA   (GEST ) GENSET.
XX
PI   Dumas Milne Edwards J,  Duclert A,  Lacroix B;
XX
DR   WPI; 1999-153778/13.
DR   P-PSDB; AAY12426.
XX
PT   New nucleic acids encoding human secreted proteins - obtained from cDNA
PT   libraries prepared from e.g. liver, ovary, brain, prostate, kidney, lung,
PT   umbilical cord, placenta and colon tissue.
XX
PS   Claim 1; Page 456; 824pp; English.
XX
CC   AAX41094 to AAX41347 represent 5' expressed sequence tags (ESTs) for
CC   human secreted proteins, and encode the proteins given in AAY12261 to
CC   AAY12514, respectively. The proteins given represent the signal peptide
CC   and an N-terminal fragment of a secreted protein. The nucleic acid
CC   sequences can be used for producing secreted human gene products. They
CC   can also be used to develop products for diagnosis and therapy. The
CC   proteins obtained may have cytokine activity, cell
CC   proliferation/differentiation activity, haematopoiesis regulating
CC   activity, tissue growth regulating activity, reproductive hormone
```

```
CC   regulating activity, chemotactic/ chemokinetic activity, haemostatic and
CC   thrombolytic activity, receptor/ ligand activity, anti-inflammatory
CC   activity, tumour inhibition activity or other activities. The products
CC   can be used in forensic, gene therapy and chromosome mapping procedures.
CC   The sequences can also be used for obtaining corresponding promoter
CC   sequences. The nucleic acids encoding the signal peptide can be used for
CC   directing extracellular secretion of a polypeptide or the insertion of a
CC   polypeptide into a membrane, or importing a polypeptide into a cell
XX
SQ   Sequence 455 BP; 102 A; 107 C; 115 G; 122 T; 0 U; 9 Other;

  Query Match             52.5%;  Score 425.2;  DB 2;  Length 455;
  Best Local Similarity   96.3%;  Pred. No. 1.6e-117;
  Matches  439;  Conservative    3;  Mismatches   12;  Indels    2;  Gaps    1;

Qy        177 GGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGC 236
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db          2 GGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGKCTGCTCCGGAGGCCGTGACGGC 61

Qy        237 CAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCTGTTGC 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCTGTTGC 121

Qy        297 CACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATAT 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 CACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATAT 181

Qy        357 TTGTAAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACAC 416
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 TTGTAAAGATCCAAAAATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACAC 241

Qy        417 AGCTCATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGA 476
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        242 AGCTCATGTTTCCTGTTTTCCAGCACCCAACATAACTTGTAAGGATNCCAGTGGCAATGA 301

Qy        477 AACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAA 536
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 AACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAA 361

Qy        537 TGGCTATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGA 596
              ||||||||||||    |:         :||||||||||||||||||||||||||||||
Db        362 TGGCTATTCCTAC--NNTKAGCAGTNNNWTGTCTCTTTTTCTTGGATGGTTGGGAGCAGA 419

Qy        597 TCGATTTTACCTTGGATACCCTGCTTTGGGTTTGTT 632
              ||||||||||||||||||||||||||||||||||
Db        420 TCGATTTTACCTTGGATACCCTGCTTTGGGTTTGTT 455
```

```
RESULT 15
AAC04131
ID   AAC04131 standard; cDNA; 487 BP.
XX
AC   AAC04131;
XX
DT   06-OCT-2000  (first entry)
XX
DE   Human secreted protein 5' EST, SEQ ID NO: 8206.
```

XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-00200610.
XX
PR 26-FEB-1999; 99US-0122487P.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR WPI; 2000-500381/45.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
PS Claim 1; SEQ ID NO 8206; 71pp + Sequence Listing; English.
XX
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used
CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors
XX
SQ Sequence 487 BP; 115 A; 118 C; 125 G; 120 T; 0 U; 9 Other;

Query Match 50.8%; Score 411.4; DB 3; Length 487;
Best Local Similarity 91.4%; Pred. No. 2.4e-113;
Matches 445; Conservative 9; Mismatches 10; Indels 23; Gaps 1;

```
Qy        164 GCGAGAAAGTGTCGGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGG 223
              |||||||||||||||||||||||||||||||:||| ||||||:||| :||| ||||
Db          1 GCGAGAAAGTGTCGGTCTCCAAGATGGCGGCCGCMTGGACGTCTGGWCCGAMTGCACCGG 60

Qy        224 AGGCCGTGACGGCCAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCT 283
              | ||||||||||||||:|||||||||||||||||||||:|||:|||||||||||||||
Db         61 AAGCCGTGACGGCCAGAMTCGTTGGTGTCCTGTGGTTCGTMTCARTCACTACAGGACCCT 120

Qy        284 GGGGGGCTGTTGCCACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAG 343
              |||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
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Db        121 GGGGGGCTGTTGCCACCTCCGCCGGGGGCRAGGAGTCGCTTAAGTGCGAGGACCTCAAAG 180

Qy        344 TGGGACAATATATT----------------------TGTAAAGATCCAAAAATAAATGA 380
              ||::|||||||  |                      |   ||||||||||||||||||
Db        181 TGRRACAATATCCTCTGTGGAGAACACCCCCCCATGGAGGCGAGATCCAAAAATAAATGA 240

Qy        381 CGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTGTTTTCCAGC 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTGTTTTCCAGC 300

Qy        441 ACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGGGAACGAAGT 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGGGAACGAAGT 360

Qy        501 TGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAAAGTGGCAGT 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAAAGTGGCAGT 420

Qy        561 CGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGGATACCCTGC 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGGATACCCTGC 480

Qy        621 TTTGGGT 627
              |||||||
Db        481 TTTGGGT 487
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Search completed: March 4, 2004, 07:39:01
Job time : 390 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 06:47:39 ; Search time 91 Seconds
(without alignments)
4939.673 Million cell updates/sec

Title: US-09-852-100B-1
Perfect score: 810
Sequence: 1 atgcatattttaaaagggtc.....aaacgcaattatatccataa 810

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	499	61.6	508	4	US-09-401-064-233	Sequence 233, App
2	499	61.6	508	4	US-09-401-064-245	Sequence 245, App
3	49.8	6.1	1455	3	US-09-276-531-33	Sequence 33, Appl
4	40.4	5.0	1119	4	US-09-489-039A-6022	Sequence 6022, Ap
5	38.6	4.8	392000	4	US-10-027-983-11	Sequence 11, Appl
6	36.8	4.5	4403765	3	US-09-103-840A-2	Sequence 2, Appli
7	36.4	4.5	1462	1	US-08-552-142A-16	Sequence 16, Appl
8	36.4	4.5	1951	1	US-08-910-973-16	Sequence 16, Appl
9	36.4	4.5	1951	4	US-09-499-227-16	Sequence 16, Appl
10	36.2	4.5	8093	4	US-10-204-708-32	Sequence 32, Appl
11	35.4	4.4	450	4	US-09-252-991A-12127	Sequence 12127, A

c	12	35.4	4.4	1404	4	US-09-252-991A-12291	Sequence 12291, A
	13	35.4	4.4	9347	4	US-10-204-708-36	Sequence 36, Appl
	14	35.4	4.4	580073	4	US-08-545-528D-1	Sequence 1, Appli
	15	35.2	4.3	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c	16	35	4.3	1494	4	US-09-252-991A-7049	Sequence 7049, Ap
	17	35	4.3	4236	4	US-09-252-991A-7057	Sequence 7057, Ap
	18	35	4.3	7304	4	US-10-204-708-43	Sequence 43, Appl
c	19	35	4.3	10023	4	US-09-252-991A-6997	Sequence 6997, Ap
	20	35	4.3	1830121	4	US-09-557-884-1	Sequence 1, Appli
	21	35	4.3	1830121	4	US-09-643-990A-1	Sequence 1, Appli
	22	34.8	4.3	832	4	US-09-621-976-2813	Sequence 2813, Ap
c	23	34.6	4.3	4673	1	US-07-638-431-1	Sequence 1, Appli
c	24	34.6	4.3	4673	5	PCT-US92-00018-1	Sequence 1, Appli
	25	34	4.2	5152	4	US-10-204-708-47	Sequence 47, Appl
	26	34	4.2	11131	4	US-10-204-708-27	Sequence 27, Appl
	27	33.6	4.1	11049	4	US-10-204-708-23	Sequence 23, Appl
c	28	33.4	4.1	549	4	US-09-252-991A-14907	Sequence 14907, A
	29	33.4	4.1	1125	4	US-09-252-991A-14723	Sequence 14723, A
	30	33.4	4.1	1636	6	5447867-2	Patent No. 5447867
c	31	33.4	4.1	1854	4	US-09-252-991A-15029	Sequence 15029, A
	32	33.4	4.1	9179	4	US-08-956-171E-100	Sequence 100, App
c	33	33.4	4.1	319608	4	US-09-539-333D-1	Sequence 1, Appli
c	34	33.4	4.1	319608	4	US-09-679-409-1	Sequence 1, Appli
c	35	33	4.1	364	4	US-09-621-976-17202	Sequence 17202, A
c	36	33	4.1	3255	4	US-09-601-198-108	Sequence 108, App
	37	33	4.1	4029	4	US-09-620-312D-201	Sequence 201, App
	38	33	4.1	5152	4	US-10-204-708-48	Sequence 48, Appl
c	39	33	4.1	55298	4	US-09-491-356C-1	Sequence 1, Appli
c	40	32.8	4.0	988	1	US-08-243-545-5	Sequence 5, Appli
c	41	32.8	4.0	988	2	US-08-993-962-5	Sequence 5, Appli
c	42	32.8	4.0	988	3	US-09-160-841-5	Sequence 5, Appli
c	43	32.8	4.0	988	3	US-09-109-100-2	Sequence 2, Appli
c	44	32.8	4.0	988	4	US-08-669-692-5	Sequence 5, Appli
c	45	32.8	4.0	988	4	US-08-444-626-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-401-064-233
; Sequence 233, Application US/09401064
; Patent No. 6623923
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeline Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C2
; CURRENT APPLICATION NUMBER: US/09/401,064
; CURRENT FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 371

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;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 233
;   LENGTH: 508
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-401-064-233

  Query Match             61.6%;  Score 499;  DB 4;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-153;
  Matches  499;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        312 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 60

Qy        372 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 120

Qy        432 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 180

Qy        492 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 240

Qy        552 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 611
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 300

Qy        612 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 360

Qy        672 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 731
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 420

Qy        732 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 791
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 480

Qy        792 AACGCAATTATATCCATAA 810
              ||||||||||||||||||
Db        481 AACGCAATTATATCCATAA 499
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RESULT 2
US-09-401-064-245
; Sequence 245, Application US/09401064
; Patent No. 6623923
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT: Lodes, Michael J.
;  APPLICANT: Secrist, Heather
;  APPLICANT: Benson, Darin R.
```

; APPLICANT: Meagher, Madeline Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C2
; CURRENT APPLICATION NUMBER: US/09/401,064
; CURRENT FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 371
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 245
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-401-064-245

Query Match 61.6%; Score 499; DB 4; Length 508;
Best Local Similarity 100.0%; Pred. No. 2.1e-153;
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        312 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 371
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Db          1 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 60

Qy        372 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 120

Qy        432 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 180

Qy        492 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 240

Qy        552 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 611
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 300

Qy        612 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 360

Qy        672 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 731
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 420

Qy        732 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 791
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Db        421 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 480

Qy        792 AACGCAATTATATCCATAA 810
              ||||||||||||||||||
Db        481 AACGCAATTATATCCATAA 499
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RESULT 3
US-09-276-531-33
; Sequence 33, Application US/09276531
; Patent No. 6183968
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Reddy, Roopa
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING
; TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL
PROLIFERATION
; NUMBER OF SEQUENCES: 134
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/276,531
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/079,677
; FILING DATE: March 27, 1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lynn E. Murry, Ph.D.
; REGISTRATION NUMBER: 42,918
; REFERENCE/DOCKET NUMBER: PA-0008 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1455 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRAITUT01
; CLONE: 746308
US-09-276-531-33

Query Match 6.1%; Score 49.8; DB 3; Length 1455;
Best Local Similarity 51.1%; Pred. No. 7.8e-06;
Matches 117; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

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Qy        504 TTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAAAGTGGCAGTCGC 563
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Db        544 TTTTCCCAAAATGCTATATTGCAATTGGACTGGAGGCTATAAGTGGTCTACGGCTCTGGC 603

Qy        564 ATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGGATACCCTGCTTT 623
              |     |    || ||  |||| |||||||| || || ||||| ||  |
Db        604 TCTAAGCATCACCCTCGGTGGGTTTGGAGCAGACCGTTTCTACCTGGGCCAGTGGCGGGA 663

Qy        624 GGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCTAATTGATTTCAT 683
              ||  |    ||| | | ||   | ||       |||||  |||  || || ||  || |
Db        664 AGGCCTCGGCAAGCTCTTCAGCTTCGGTGGCCTGGGAATATGGACGCTGATAGACGTCCT 723

Qy        684 TCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACATT 732
              || |||  | |      |||||||| |||||||   |   ||||||
Db        724 GCTCATTGGAGTTGGCTATGTTGGACCAGCAGATGGCTCTTTGTACATT 772
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RESULT 4
US-09-489-039A-6022
; Sequence 6022, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 6022
; LENGTH: 1119
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6022

Query Match 5.0%; Score 40.4; DB 4; Length 1119;
Best Local Similarity 50.0%; Pred. No. 0.0079;
Matches 101; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

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Qy        105 GAACCTCGCCCTGTTGCCCTTCTCCCTCCCGCTCCTGGGCGGAGGCGGAAGCGGAAGTGG 164
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Qy        165 CGAGAAAGTGTCGGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGA 224
              |||   || | | | | ||  || |||  | |||       |    ||  | || || |
Db        732 CGAACCAGCGGCAGCCGCCGCGACGGCTCCTGCCGCCGGCGCCACGCCAACAGCGCCAGT 791

Qy        225 GGCCGTGACGGCCAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTG 284
              | ||| | | | |    |    |||    ||  |  ||   | | |||  | | | ||
Db        792 GACCGCGCCTGGCTCCATTCAGGGTAATGTGGCGCCCGCTGCGGCCACCGCCGCAGCCGC 851

Qy        285 GGGGGCTGTTGCCACCTCCGCC 306
               || || ||  ||  ||||  ||
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Db 852 TGGCGCCGTGGCGGCCTCGTCC 873

RESULT 5
US-10-027-983-11
; Sequence 11, Application US/10027983
; Patent No. 6617162
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Mark P. Roach
; TITLE OF INVENTION: ANTISENSE MODULATION OF ESTROGEN RECEPTOR ALPHA EXPRESSION
; FILE REFERENCE: RTS-0340
; CURRENT APPLICATION NUMBER: US/10/027,983
; CURRENT FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 11
; LENGTH: 392000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 137740
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 137742
; OTHER INFORMATION: unknown
; NAME/KEY: misc_feature
; LOCATION: (138122)...(138221)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: unsure
; LOCATION: 145507
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 151967
; OTHER INFORMATION: unknown
; NAME/KEY: misc_feature
; LOCATION: (151967)...(1542066)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: unsure
; LOCATION: 154217
; OTHER INFORMATION: unknown
; NAME/KEY: misc_feature
; LOCATION: (164037)...(164136)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc_feature
; LOCATION: (174657)...(174756)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc_feature
; LOCATION: (186224)...(186323)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc_feature
; LOCATION: (195242)...(195341)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: unsure
; LOCATION: 202703
; OTHER INFORMATION: unknown

; NAME/KEY: misc_feature
; LOCATION: (202771)...(202870)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc_feature
; LOCATION: (206246)...(215602)
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; NAME/KEY: misc_feature
; LOCATION: (218126)...(218225)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc_feature
; LOCATION: (220360)...(220459)
; OTHER INFORMATION: n = A,T,C or G
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; LOCATION: (222717)...(222816)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc_feature
; LOCATION: (223981)...(224080)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc_feature
; LOCATION: (227487)...(227586)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc_feature
; LOCATION: (230157)...(230256)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc_feature
; LOCATION: (232299)...(232398)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc_feature
; LOCATION: (236552)...(2366651)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc_feature
; LOCATION: (238789)...(248788)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: exon
; LOCATION: (118288)...(119101)
; OTHER INFORMATION: exon 1C
; NAME/KEY: exon:intron junction
; LOCATION: (151129)...(151130)
; OTHER INFORMATION: exon 5:intron 5
; NAME/KEY: exon:intron junction
; LOCATION: (299248)...(299249)
; OTHER INFORMATION: exon 9:intron 9
; NAME/KEY: exon:intron junction
; LOCATION: (348578)...(348579)
; OTHER INFORMATION: exon 10:intron 10
; NAME/KEY: intron
; LOCATION: (348579)...(381838)
; OTHER INFORMATION: intron 10
; NAME/KEY: intron:exon junction
; LOCATION: (386185)...(386186)
; OTHER INFORMATION: intron 11:exon 12
US-10-027-983-11

  Query Match   4.8%; Score 38.6; DB 4; Length 392000;
  Best Local Similarity   54.6%; Pred. No. 1.5;
  Matches   77; Conservative   0; Mismatches   64; Indels   0; Gaps   0;

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Qy        237 CAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCTGTTGC 296
              || | | |   | || | |  | || |  | ||||  ||| ||  || ||  |||  |
Db     127492 CAAATTTGGCTGCGTGCAGCTGCTCATGCCTGTCATCCCAGCACTTTGAGGAACTGAAGG
127551

Qy        297 CACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATAT 356
               |    ||  | | | ||||||  |  |   ||  || |  || |||| |||  | | |
Db     127552 GAGGATTGCTTGAGTCCAGGAGTTCCAGACCAGCCTGGGCAACACAGTGAGACCCTGTCT
127611

Qy        357 TTGTAAAGATCCAAAAATAAA 377
               |  ||| |  |||||| |||
Db     127612 CTACAAAAAAACAAAAACAAA 127632
```

RESULT 6
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 4403765
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   FEATURE:
;   OTHER INFORMATION: CDC 1551
;   OTHER INFORMATION: "n" bases at various positions throughout the sequence
;   OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

  Query Match   4.5%; Score 36.8; DB 3; Length 4403765;
  Best Local Similarity   47.8%; Pred. No. 25;
  Matches 107; Conservative   0; Mismatches 117; Indels   0; Gaps   0;

```
Qy        112 GCCCTGTTGCCCTTCTCCCTCCCGCTCCTGGGCGGAGGCGGAAGCGGAAGTGGCGAGAAA 171
              |||  |   ||  |   |  |  ||  |  ||  |  ||   |||  |  ||||  |
Db     676161 GCCGGGCGCGCCGTTCGCGCCATGCGCGCTGCCGCCGACGCTGGCGCCACCGGCGCCACC
676220

Qy        172 GTGTCGGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTG 231
              |   |   |  |     ||  ||||||    |  | |||||  | |   || |||  |||
Db     676221 GGCCCCACCGGCGCCCGGGTTGCCGCCATTGCCACCGGTCCCGCCGGCACGAAGGTTGTG
676280

Qy        232 ACGGCCAGACTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCT 291
              ||  |  | | ||  | | | | |      ||||  | |  |   | |    |   |  |||
```

```
Db      676281 ACCCCACGTCCCGGTAGCGCCGTTGCCGCCGTCACCGGGAGCTCCGCCGTCACCGCCGCT
676340

Qy         292 GTTGCCACCTCCGCCGGGGGCGAGGAGTCGCTTAAGTGCGAGGA 335
                |||| | ||||||| | || ||   |     ||  |||| |
Db      676341 ACCGCCAGCCCCGCCGGCGCCGTGGCTGCCGCCGAGGCCGAGCA 676384


RESULT 7
US-08-552-142A-16
; Sequence 16, Application US/08552142A
; Patent No. 5695995
;  GENERAL INFORMATION:
;    APPLICANT:  Weintraub, Harold M.
;    APPLICANT:  Lee, Jacqueline E.
;    APPLICANT:  Tapscott, Stephen J.
;    APPLICANT:  Hollenberg, Stanley M.
;    TITLE OF INVENTION:  Neurogenic Differentiation (NeuroD) Genes
;    TITLE OF INVENTION:  and Proteins
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Christensen O'Connor Johnson KindnessPLLC
;      STREET:  1420 Fifth Avenue, Suite 2800
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101-2347
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/552,142A
;      FILING DATE:  02-NOV-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/239,238
;      FILING DATE:  06-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US95/05741
;      FILING DATE:  08-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Broderick, Thomas F.
;      REGISTRATION NUMBER:  31,332
;      REFERENCE/DOCKET NUMBER:  FHCR-1-8933
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-682-8100
;      TELEFAX:  206-225-0709
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1462 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
```

```
;       ORGANISM:  Mus musculus
;     IMMEDIATE SOURCE:
;       CLONE:  1.1.1
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  231..1101
US-08-552-142A-16

  Query Match              4.5%;  Score 36.4;  DB 1;  Length 1462;
  Best Local Similarity   49.0%;  Pred. No. 0.19;
  Matches   97;  Conservative    0;  Mismatches  101;  Indels    0;  Gaps    0;

Qy         121 CCCTTCTCCCTCCCGCTCCTGGGCGGAGGCGGAAGCGGAAGTGGCGAGAAAGTGTCGGTC 180
               | | ||||   |  || |  |  ||   || |  |||   | | |||  | | | ||
Db         261 CTCCTCTCGGACGTGCCCAAGTTCGCCAGCTGGGGCGACGGCGACGACGACGAGCCGAGG 320

Qy         181 TCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGCCAGA 240
                 | | | ||  | |||   ||||     | |  ||||||| | | | | | |  |  ||
Db         321 AGCGACAAGGGCGACGCGCCGCCGCAGCCTTCTCCTGCTCCCGGGTCGGGGGCTCCAGGA 380

Qy         241 CTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCTGTTGCCACC 300
               | ||   | | |     |   || ||  |   |  ||||     |    |||   ||||
Db         381 CCCGCCCGGGCCGCCAAGCCAGTGTCTCTTCGTGGAGGAGAAGAGATCCCTGAACCCACG 440

Qy         301 TCCGCCGGGGGCGAGGAG 318
               |  || | || | |||||
Db         441 TTGGCTGAGGTCAAGGAG 458


RESULT 8
US-08-910-973-16
; Sequence 16, Application US/08910973
; Patent No. 5795723
;  GENERAL INFORMATION:
;    APPLICANT:  Tapscott, Stephen J.
;    APPLICANT:  Olson, James M.
;    TITLE OF INVENTION:  Expression of Neurogenic bHLH Genes in Primitive
Neuroectoder
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Christensen O'Connor Johnson KindnessPLLC
;      STREET:  1420 Fifth Avenue, Suite 2800
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101-2347
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/910,973
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/239,238
```

```
;      FILING DATE:  06-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US95/05741
;      FILING DATE:  08-MAY-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/17532
;      FILING DATE:  30-October-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sheiness, Diana K.
;      REGISTRATION NUMBER:  35,356
;      REFERENCE/DOCKET NUMBER:  FHCR-1-10958
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-682-8100; 206-224-0735 (direct)
;      TELEFAX:  206-225-0779
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1951 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Mus musculus
;    IMMEDIATE SOURCE:
;      CLONE:  1.1.1 (mouse neuroD2)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  230..1378
US-08-910-973-16

  Query Match             4.5%;  Score 36.4;  DB 1;  Length 1951;
  Best Local Similarity   49.0%;  Pred. No. 0.23;
  Matches   97;  Conservative    0;  Mismatches  101;  Indels    0;  Gaps    0;

Qy        121 CCCTTCTCCCTCCCGCTCCTGGGCGGAGGCGGAAGCGGAAGTGGCGAGAAAGTGTCGGTC 180
              | | ||||   |  || |  |  ||   || |  |||   | | |||  | | | ||
Db        260 CTCCTCTCGGACGTGCCCAAGTTCGCCAGCTGGGGCGACGGCGACGACGACGAGCCGAGG 319

Qy        181 TCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGCCAGA 240
                | | | ||  | |||   ||||     | |  ||||||| | | | | | |  |  ||
Db        320 AGCGACAAGGGCGACGCGCCGCCGCAGCCTTCTCCTGCTCCCGGGTCGGGGGCTCCAGGA 379

Qy        241 CTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCTGTTGCCACC 300
              | ||   | | |     |   || ||  |   |  ||||     |    |||   ||||
Db        380 CCCGCCCGGGCCGCCAAGCCAGTGTCTCTTCGTGGAGGAGAAGAGATCCCTGAACCCACG 439

Qy        301 TCCGCCGGGGGCGAGGAG 318
              |  || | || | |||||
Db        440 TTGGCTGAGGTCAAGGAG 457


RESULT 9
US-09-499-227-16
; Sequence 16, Application US/09499227
; Patent No. 6444463
;  GENERAL INFORMATION:
;    APPLICANT:  Tapscott, Stephen J.
```

```
;    APPLICANT:  Olson, James M.
;    TITLE OF INVENTION:  Expression of Neurogenic bHLH Genes in Primitive
Neuroectoder
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Christensen O'Connor Johnson KindnessPLLC
;      STREET:  1420 Fifth Avenue, Suite 2800
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101-2347
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/499,227
;      FILING DATE:  05-August-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/239,238
;      FILING DATE:  06-May-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US95/05741
;      FILING DATE:  08-May-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/17532
;      FILING DATE:  30-October-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/910,973
;      FILING DATE:  07-August-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sheiness, Diana K.
;      REGISTRATION NUMBER:  35,356
;      REFERENCE/DOCKET NUMBER:  FHCR-1-12742
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-682-8100; 206-224-0735 (direct)
;      TELEFAX:  206-225-0779
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1951 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Mus musculus
;    IMMEDIATE SOURCE:
;      CLONE:  1.1.1 (mouse neuroD2)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  230..1378
US-09-499-227-16

  Query Match              4.5%;  Score 36.4;  DB 4;  Length 1951;
  Best Local Similarity   49.0%;  Pred. No. 0.23;
  Matches   97;  Conservative    0;  Mismatches  101;  Indels    0;  Gaps    0;
```

```
Qy        121 CCCTTCTCCCTCCCGCTCCTGGGCGGAGGCGGAAGCGGAAGTGGCGAGAAAGTGTCGGTC 180
              | | ||||   |  || |  |  ||   || |  |||   | | |||  | | | ||
Db        260 CTCCTCTCGGACGTGCCCAAGTTCGCCAGCTGGGGCGACGGCGACGACGACGAGCCGAGG 319

Qy        181 TCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGCCAGA 240
                | | | ||  | |||   ||||     | |  ||||||| | | | | | |  | ||
Db        320 AGCGACAAGGGCGACGCGCCGCCGCAGCCTTCTCCTGCTCCCGGGTCGGGGGCTCCAGGA 379

Qy        241 CTCGTTGGTGTCCTGTGGTTCGTCTCAGTCACTACAGGACCCTGGGGGGCTGTTGCCACC 300
              | ||   | | |     |   || ||  |   |  ||||     |    |||   ||||
Db        380 CCCGCCCGGGCCGCCAAGCCAGTGTCTCTTCGTGGAGGAGAAGAGATCCCTGAACCCACG 439

Qy        301 TCCGCCGGGGGCGAGGAG 318
              |  || | || | |||||
Db        440 TTGGCTGAGGTCAAGGAG 457


RESULT 10
US-10-204-708-32
; Sequence 32, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
;  APPLICANT: OLEK, Alexander
;  APPLICANT:  PIEPENBROCK, Christian
;  APPLICANT:  BERLIN, Kurt
;  TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
;  TITLE OF INVENTION:  by Assessing DNA Methylation
;  FILE REFERENCE: 5013.1012
;  CURRENT APPLICATION NUMBER: US/10/204,708
;  CURRENT FILING DATE:  2003-05-06
;  PRIOR APPLICATION NUMBER: PCT/EP01/03971
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: DE 10019058.8
;  PRIOR FILING DATE: 2000-04-06
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: DE 10032529.7
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: DE 10043826.1
;  PRIOR FILING DATE: 2000-09-01
;  NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 32
;   LENGTH: 8093
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-32

  Query Match             4.5%;  Score 36.2;  DB 4;  Length 8093;
  Best Local Similarity   54.0%;  Pred. No. 0.69;
  Matches   74;  Conservative    0;  Mismatches   63;  Indels    0;  Gaps    0;

Qy        673 ATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACATT 732
              | | ||||  |  || | | ||   |  |||||     || | || | | |  ||| |||
Db       6468 AGTAATTTTGTATTTTTATTAAGATAATTTGTTTTGTGTTAAAATAGTAATTTTTAAATT 6527
```

```
Qy        733 ATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAAA 792
              | | ||| |||| ||    | ||  ||   | | |||    ||| ||  ||  | |  |
Db       6528 TTTGTTTATTATGAAAAGGTAATTTTAAAGTTTATTATGTAAAATTAATTATAAATAGGA 6587

Qy        793 ACGCAATTATATCCATA 809
                | ||||||  |||
Db       6588 TTTAATTTATATTTATA 6604
```

RESULT 11
US-09-252-991A-12127
; Sequence 12127, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12127
; LENGTH: 450
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12127

Query Match 4.4%; Score 35.4; DB 4; Length 450;
Best Local Similarity 48.3%; Pred. No. 0.19;
Matches 99; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

```
Qy         60 GCGAAGAGACGGAACTGGCCTCTATCCTATGCGAGGTCCCTTTAAGAACCTCGCCCTGTT 119
              ||| ||  | |  ||   |||    |     |   ||| |     | |   ||  | | |
Db         45 GCGCAGCCAGGTCACCACCCTGACCCGCCGCCTGCGTCGCGAGGCGCAGGCCGATCCGGT 104

Qy        120 GCCCTTCTCCCTCCCGCTCCTGGGCGGAGGCGGAAGCGGAAGTGGCGAGAAAGTGTCGGT 179
              ||  ||||| |  | | || ||   || |       | |   |||||   | ||  |
Db        105 GCAATTCTCGCAACTGGTCGTGCTTGGCGCGATCGACCGCCTTGGCGGCGACGTCACACC 164

Qy        180 CTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGCCAG 239
              ||| ||-|||| |||||| -||-|-----|-|||| -||-||--||--||-|-|-
Db        165 TTCCGAGCTGGCCGCCGCCGAGCGGATGCGCTCGTCGAATCTGGCCGCGCTGCTGCGCGA 224

Qy        240 ACTCGTTGGTGTCCTGTGGTTCGTC 264
              ||| |   | |    |  | |||||
Db        225 ACTGGAACGCGGAGGGCTGATCGTC 249
```

RESULT 12
US-09-252-991A-12291/c
; Sequence 12291, Application US/09252991A

; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12291
; LENGTH: 1404
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12291

Query Match 4.4%; Score 35.4; DB 4; Length 1404;
Best Local Similarity 48.3%; Pred. No. 0.4;
Matches 99; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

```
Qy          60 GCGAAGAGACGGAACTGGCCTCTATCCTATGCGAGGTCCCTTTAAGAACCTCGCCCTGTT 119
               ||| ||  | |  ||   |||    |     |   ||| |     | |   ||  | | |
Db        1324 GCGCAGCCAGGTCACCACCCTGACCCGCCGCCTGCGTCGCGAGGCGCAGGCCGATCCGGT 1265

Qy         120 GCCCTTCTCCCTCCCGCTCCTGGGCGGAGGCGGAAGCGGAAGTGGCGAGAAAGTGTCGGT 179
               ||  ||||| |  | | || ||   || |       | |   |||||   | ||  |
Db        1264 GCAATTCTCGCAACTGGTCGTGCTTGGCGCGATCGACCGCCTTGGCGGCGACGTCACACC 1205

Qy         180 CTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGCCAG 239
                ||| || |||| ||||||  || |    | ||||   || ||  ||  ||  |  |
Db        1204 TTCCGAGCTGGCCGCCGCCGAGCGGATGCGCTCGTCGAATCTGGCCGCGCTGCTGCGCGA 1145

Qy         240 ACTCGTTGGTGTCCTGTGGTTCGTC 264
               ||| |   | |    |  | |||||
Db        1144 ACTGGAACGCGGAGGGCTGATCGTC 1120
```

RESULT 13
US-10-204-708-36
; Sequence 36, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8

; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 36
;   LENGTH: 9347
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-36

  Query Match   4.4%; Score 35.4; DB 4; Length 9347;
  Best Local Similarity   45.7%; Pred. No. 1.4;
  Matches 123; Conservative   0; Mismatches 146; Indels   0; Gaps   0;

```
Qy        535 AATGGCTATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCA 594
              ||| |   ||   | ||| | | |||    || | || ||   |   ||  ||      |
Db       7248 AATAGTAGTTGAGATAAAATAGAAGTTTATTTTTTTCGTTAGATAAAATAATTTTAGAGA 7307

Qy        595 GATCGATTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTT 654
               |   | ||||   |  | |   || |||    ||  | | |||||   |  |    |||
Db       7308 TAGGTAGTTTAGGGTTAAAATGGTGGTTTTACGTTTATTAGGTTTTTATCGTTTTATTTT 7367

Qy        655 TGTGGAATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCA 714
                ||   | |       |  ||  ||| ||  |||||| | ||   |   | |    |  |
Db       7368 ATTGTTTTCGAATTAATTTTTATTTTTATAGTTATTTTATTGTTTAAGATGGTTTTTGGA 7427

Qy        715 GATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACT 774
                |  |  || |    |||||  ||| | | |     |      | ||   || |    |
Db       7428 ATTTTAGTTATTAGATTTATATTTTATTTTAGGTAGCGGAAAGTAGGAAGAAGAAAGGGT 7487

Qy        775 AATGAAACATTTAGAAAAACGCAATTATA 803
              ||  |||  |||| ||| |   | | | |
Db       7488 AAATAAAATTTTAAAAATATAAAGTAAGA 7516
```

RESULT 14
US-08-545-528D-1
; Sequence 1, Application US/08545528D
; Patent No. 6537773
; GENERAL INFORMATION:
; APPLICANT: Fraser et al.
; TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome,
Fragments
; Patent No. 6537773
; TITLE OF INVENTION: Thereof, and Uses Thereof
; FILE REFERENCE: PB193P1
; CURRENT APPLICATION NUMBER: US/08/545,528D
; CURRENT FILING DATE: 1995-10-19
; PRIOR APPLICATION NUMBER: US 08/488,018
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/473,545

```
;  PRIOR FILING DATE: 1995-06-07
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 580073
;   TYPE: DNA
;   ORGANISM: Mycoplasma genitalium
US-08-545-528D-1

  Query Match             4.4%;  Score 35.4;  DB 4;  Length 580073;
  Best Local Similarity   55.2%;  Pred. No. 21;
  Matches   69;  Conservative    0;  Mismatches   56;  Indels    0;  Gaps    0;

Qy        685 CTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACATTATAGATTACTAT 744
              ||| ||| ||   | |||||    | ||  ||    |       ||  || || |  |
Db     387060 CTTTTTTAAAGTTAAATTGTCCTGCTTTGTGAATCCATGGTAAGCAGGATGGAATTATTA
387119

Qy        745 GGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAAAACGCAATTATAT 804
               | |||   | | |||| || | ||| | | || ||||| | || |||    | ||| |
Db     387120 AGTACCTTCCATCCAAGGCTTATTATGAATCATTAAACAATAAGCAAATTCAATTTAAAG
387179

Qy        805 CCATA 809
              |||||
Db     387180 CCATA 387184


RESULT 15
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 4411529
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   OTHER INFORMATION: H37Rv
US-09-103-840A-1

  Query Match             4.3%;  Score 35.2;  DB 3;  Length 4411529;
  Best Local Similarity   47.3%;  Pred. No. 66;
  Matches  106;  Conservative    0;  Mismatches  118;  Indels    0;  Gaps    0;

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 08:34:04 ; Search time 349 Seconds
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Title: US-09-852-100B-1
Perfect score: 810
Sequence: 1 atgcatattttaaaagggtc.....aaacgcaattatatccataa 810

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2421054 seqs, 1828716029 residues

Total number of hits satisfying chosen parameters: 4842108

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	810	100.0	810	9	US-09-833-503A-1	Sequence 1, Appli
	3	810	100.0	810	14	US-10-199-881-1	Sequence 1, Appli
	4	499	61.6	508	9	US-09-922-217-233	Sequence 233, App
	5	499	61.6	508	9	US-09-922-217-245	Sequence 245, App
	6	499	61.6	508	9	US-09-833-263-233	Sequence 233, App
	7	499	61.6	508	9	US-09-833-263-245	Sequence 245, App
	8	499	61.6	508	13	US-10-025-380-233	Sequence 233, App
	9	499	61.6	508	13	US-10-025-380-245	Sequence 245, App
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	37	48.8	6.0	423	14	US-10-198-846-8649	Sequence 8649, Ap
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	40	39.8	4.9	909	14	US-10-156-761-6614	Sequence 6614, Ap
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	42	39.8	4.9	962	14	US-10-199-881-3	Sequence 3, Appli
	43	39.8	4.9	1409	9	US-09-925-301-176	Sequence 176, App
	44	39.8	4.9	1422	10	US-09-798-889-24	Sequence 24, Appl
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ALIGNMENTS

RESULT 1
US-09-852-100A-1
; Sequence 1, Application US/09852100A
; Patent No. US20020058267A1
; GENERAL INFORMATION:
; APPLICANT: American Home Products

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;  TITLE OF INVENTION: Beta-amyloid Peptide-Binding Proteins and Polynucleotides
Encoding the
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE: AHP981261p2
;  CURRENT APPLICATION NUMBER: US/09/852,100A
;  CURRENT FILING DATE:  2001-05-09
;  PRIOR APPLICATION NUMBER: US 09/172,990
;  PRIOR FILING DATE: 1998-10-14
;  PRIOR APPLICATION NUMBER: US 60/104,104
;  PRIOR FILING DATE: 1998-10-13
;  PRIOR APPLICATION NUMBER: PTC/US99/21621
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: US 09/060,609
;  PRIOR FILING DATE: 1998-04-15
;  PRIOR APPLICATION NUMBER: US 60/064,583
;  PRIOR FILING DATE: 1997-04-16
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 810
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(807)
US-09-852-100A-1

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  Best Local Similarity   100.0%;  Pred. No. 1.8e-244;
  Matches  810;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 2
US-09-833-503A-1
; Sequence 1, Application US/09833503A
; Patent No. US20020146760A1
; GENERAL INFORMATION:
; APPLICANT: Ozenberger, Bradley A
; APPLICANT: Kajkowski, Eileen M
; APPLICANT: Lo, Ching-Hsiung F
; APPLICANT: American Home Products Corporation
; TITLE OF INVENTION: No. US20020146760A1el G-Protein-Coupled Receptor-Like Proteins and
; TITLE OF INVENTION: Polynucleotides Encoded By Them, and Methods of Using
; TITLE OF INVENTION: Same
; FILE REFERENCE: AHP98165-00PCT
; CURRENT APPLICATION NUMBER: US/09/833,503A
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/104,104
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 810
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-503A-1

Query Match 100.0%; Score 810; DB 9; Length 810;
Best Local Similarity 100.0%; Pred. No. 1.8e-244;
Matches 810; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
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; Sequence 1, Application US/10199881
; Publication No. US20030096356A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  TITLE OF INVENTION: No. US20030096356A1el G-Protein-Coupled Receptor-Like
Proteins and Polynucleotides
;  TITLE OF INVENTION:  Encoded by Them, and Methods of Using Same"
;  FILE REFERENCE: AHP98165C1
;  CURRENT APPLICATION NUMBER: US/10/199,881
;  CURRENT FILING DATE:  2002-07-18
;  PRIOR APPLICATION NUMBER: PCT/ US99/21621
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: US 90/833,5081
;  PRIOR FILING DATE: 2001-12-04
;  PRIOR APPLICATION NUMBER: US 60/104,104
;  PRIOR FILING DATE: 1998-10-13
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
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;   TYPE: DNA
;   ORGANISM: Homo sapiens
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;   NAME/KEY: CDS
;   LOCATION: (1)..(810)
;   OTHER INFORMATION:
US-10-199-881-1

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Db        481 CATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGC 540

Qy        541 TATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGA 600

Qy        601 TTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGA 660

Qy        661 ATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGA 720

Qy        721 AGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAA 780

Qy        781 ACATTTAGAAAAACGCAATTATATCCATAA 810
              ||||||||||||||||||||||||||||||
Db        781 ACATTTAGAAAAACGCAATTATATCCATAA 810
```

RESULT 4
US-09-922-217-233
; Sequence 233, Application US/09922217
; Patent No. US20020076414A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole Lynn
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE

; FILE REFERENCE: 210121.471C13
; CURRENT APPLICATION NUMBER: US/09/922,217
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 233
;   LENGTH: 508
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-922-217-233

  Query Match   61.6%; Score 499; DB 9; Length 508;
  Best Local Similarity   100.0%; Pred. No. 1.8e-146;
  Matches 499; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy        312 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 60

Qy        372 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 120

Qy        432 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 180

Qy        492 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 240

Qy        552 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 611
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 300

Qy        612 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 360

Qy        672 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 731
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 420

Qy        732 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 791
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 480

Qy        792 AACGCAATTATATCCATAA 810
              ||||||||||||||||||
Db        481 AACGCAATTATATCCATAA 499
```

RESULT 5
US-09-922-217-245
; Sequence 245, Application US/09922217
; Patent No. US20020076414A1
; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole Lynn
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C13
; CURRENT APPLICATION NUMBER: US/09/922,217
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 245
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-217-245

Query Match 61.6%; Score 499; DB 9; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.8e-146;
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        312 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 60

Qy        372 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 120

Qy        432 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 180

Qy        492 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 240

Qy        552 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 611
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 300

Qy        612 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 360

Qy        672 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 731
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 420
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```
Qy        732 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 791
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 480

Qy        792 AACGCAATTATATCCATAA 810
              ||||||||||||||||||
Db        481 AACGCAATTATATCCATAA 499
```

RESULT 6
US-09-833-263-233
; Sequence 233, Application US/09833263
; Patent No. US20020110547A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Stolk, John A.
; APPLICANT: Meagher, Madeleine J.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C12
; CURRENT APPLICATION NUMBER: US/09/833,263
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 233
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-833-263-233

Query Match 61.6%; Score 499; DB 9; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.8e-146;
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        312 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 60

Qy        372 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 120

Qy        432 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 180

Qy        492 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 240

Qy        552 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 611
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 300

Qy        612 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        301 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 360

Qy        672 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 731
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 420

Qy        732 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 791
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 480

Qy        792 AACGCAATTATATCCATAA 810
              ||||||||||||||||||
Db        481 AACGCAATTATATCCATAA 499
```

RESULT 7
US-09-833-263-245
; Sequence 245, Application US/09833263
; Patent No. US20020110547A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Stolk, John A.
; APPLICANT: Meagher, Madeleine J.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C12
; CURRENT APPLICATION NUMBER: US/09/833,263
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 245
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-833-263-245

Query Match 61.6%; Score 499; DB 9; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.8e-146;
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        312 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 60

Qy        372 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 120

Qy        432 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 180

Qy        492 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 240
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```
Qy        552 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 611
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 300

Qy        612 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 360

Qy        672 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 731
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 420

Qy        732 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 791
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 480

Qy        792 AACGCAATTATATCCATAA 810
              ||||||||||||||||||
Db        481 AACGCAATTATATCCATAA 499
```

RESULT 8
US-10-025-380-233
; Sequence 233, Application US/10025380
; Publication No. US20020182191A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025,380
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 1129
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 233
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-025-380-233

Query Match 61.6%; Score 499; DB 13; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.8e-146;

```
  Matches  499;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        312 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 60

Qy        372 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 120

Qy        432 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 180

Qy        492 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 240

Qy        552 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 611
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 300

Qy        612 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 360

Qy        672 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 731
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 420

Qy        732 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 791
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 480

Qy        792 AACGCAATTATATCCATAA 810
              ||||||||||||||||||
Db        481 AACGCAATTATATCCATAA 499


RESULT 9
US-10-025-380-245
; Sequence 245, Application US/10025380
; Publication No. US20020182191A1
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Lodes, Michael J.
;  APPLICANT:  Secrist, Heather
;  APPLICANT:  Benson, Darin R.
;  APPLICANT:  Meagher, Madeleine Joy
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Smith, Carole L.
;  APPLICANT:  King, Gordon E.
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Clapper, Jonathan D.
;  APPLICANT:  Skeiky, Yasir A. W.
```

; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025,380
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 1129
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 245
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-025-380-245

Query Match 61.6%; Score 499; DB 13; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.8e-146;
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        312 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGGACAATATATTTGTAAAGATCCAAA 60

Qy        372 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATAAATGACGCTACGCAAGAACCAGTTAACTGTACAAACTACACAGCTCATGTTTCCTG 120

Qy        432 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTTACTGG 180

Qy        492 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCTACAA 240

Qy        552 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 611
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGAGCAGATCGATTTTACCTTGG 300

Qy        612 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGGTTTTGTGGAATTGGGAGCCT 360

Qy        672 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 731
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 420

Qy        732 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 791
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 480

Qy        792 AACGCAATTATATCCATAA 810
              ||||||||||||||||||
Db        481 AACGCAATTATATCCATAA 499
```

RESULT 10
US-09-918-995-6918
; Sequence 6918, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6918
;   LENGTH: 431
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(431)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-6918

  Query Match 41.7%; Score 337.4; DB 10; Length 431;
  Best Local Similarity 99.7%; Pred. No. 1.5e-95;
  Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy        472 AATGAAACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAAT 531
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AATGAAACACATTTTACTGGGAACGAAGTTGGTTTTTTCAAGCCCATATCTTGCCGAAAT 60

Qy        532 GTAAATGGCTATTCCTACAAAGTGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGA 591
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db         61 GTAAATGGCTATTCCTACAAAGAGGCAGTCGCATTGTCTCTTTTTCTTGGATGGTTGGGA 120

Qy        592 GCAGATCGATTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGG 651
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCAGATCGATTTTACCTTGGATACCCTGCTTTGGGTTTGTTAAAGTTTTGCACTGTAGGG 180

Qy        652 TTTTGTGGAATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCT 711
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTTTGTGGAATTGGGAGCCTAATTGATTTCATTCTTATTTCAATGCAGATTGTTGGACCT 240

Qy        712 TCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATT 771
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATT 300

Qy        772 ACTAATGAAACATTTAGAAAAACGCAATTATATCCATAA 810
              |||||||||||||||||||||||||||||||||||||
Db        301 ACTAATGAAACATTTAGAAAAACGCAATTATATCCATAA 339
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RESULT 11
US-10-085-783A-36056
; Sequence 36056, Application US/10085783A

; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36056
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13)..(13)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (30)..(30)
; OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-36056

Query Match 12.3%; Score 100; DB 12; Length 256;
Best Local Similarity 99.1%; Pred. No. 8.7e-21;
Matches 111; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy        700 ATTGTTGGACCTTCAG-ATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTAC 758
              ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db         14 ATTGTTGGACCTTCAGNATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTAC 73

Qy        759 AAGACTGAGTATTACTAATGAAACATTTAGAAAAACGCAATTATATCCATAA 810
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         74 AAGACTGAGTATTACTAATGAAACATTTAGAAAAACGCAATTATATCCATAA 125
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RESULT 12
US-10-242-535A-36056
; Sequence 36056, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A

; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36056
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13)..(13).
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (30)..(30)
; OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-36056

Query Match 12.3%; Score 100; DB 15; Length 256;
Best Local Similarity 99.1%; Pred. No. 8.7e-21;
Matches 111; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
Qy        700 ATTGTTGGACCTTCAG-ATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTAC 758
              ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db         14 ATTGTTGGACCTTCAGNATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTAC 73

Qy        759 AAGACTGAGTATTACTAATGAAACATTTAGAAAAACGCAATTATATCCATAA 810
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         74 AAGACTGAGTATTACTAATGAAACATTTAGAAAAACGCAATTATATCCATAA 125
```

RESULT 13
US-10-085-783A-48351
; Sequence 48351, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12

; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48351
;   LENGTH: 411
;   TYPE: DNA
;   ORGANISM: Human
US-10-085-783A-48351

  Query Match   10.5%; Score 85.4; DB 12; Length 411;
  Best Local Similarity   98.9%; Pred. No. 4.8e-16;
  Matches   86; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   724 AGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACA 783
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 AGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACA 60

Qy   784 TTTAGAAAAACGCAATTATATCCATAA 810
              |||||||||||||| ||||||||||||
Db   61 TTTAGAAAAACGCAGTTATATCCATAA 87

RESULT 14
US-10-242-535A-48351
; Sequence 48351, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48351
;   LENGTH: 411
;   TYPE: DNA
;   ORGANISM: Human
US-10-242-535A-48351

  Query Match   10.5%; Score 85.4; DB 15; Length 411;
  Best Local Similarity   98.9%; Pred. No. 4.8e-16;
  Matches   86; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   724 AGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACA 783
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 AGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACA 60

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Qy        784 TTTAGAAAAACGCAATTATATCCATAA 810
              ||||||||||||| ||||||||||||
Db         61 TTTAGAAAAACGCAGTTATATCCATAA 87
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RESULT 15
US-10-085-783A-16414
; Sequence 16414, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16414
; LENGTH: 129
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-16414

Query Match 9.8%; Score 79; DB 12; Length 129;
Best Local Similarity 89.5%; Pred. No. 2.3e-14;
Matches 85; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

```
Qy        716 ATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTA 775
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db          1 ATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTTAGTATTACTA 60

Qy        776 ATGAAACATTTAGAAAAACGCAATTATATCCATAA 810
              |   ||   ||   ||||||||||||||||||||
Db         61 AGTGAAACATTTAGAAAACGCAATTATATCCATAA 95
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Search completed: March 4, 2004, 10:22:21
Job time : 351 secs